

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on: September 28, 2001, 10:28:10 ; Search time 34.79 Seconds
(without alignments)
592.474 Million cell updates/sec

Title: US-09-492-029-3
Sequence: 1 MGEMEQLEKQAEQLEKQIAD.....TADGMAVATGSMDSFLKIWN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601:*

1:	/SID88/gcgdata/geneseq/geneseq/AA1980.DAT:*
2:	/SID88/gcgdata/geneseq/geneseq/AA1981.DAT:*
3:	/SID88/gcgdata/geneseq/geneseq/AA1982.DAT:*
4:	/SID88/gcgdata/geneseq/geneseq/AA1983.DAT:*
5:	/SID88/gcgdata/geneseq/geneseq/AA1984.DAT:*
6:	/SID88/gcgdata/geneseq/geneseq/AA1985.DAT:*
7:	/SID88/gcgdata/geneseq/geneseq/AA1986.DAT:*
8:	/SID88/gcgdata/geneseq/geneseq/AA1987.DAT:*
9:	/SID88/gcgdata/geneseq/geneseq/AA1988.DAT:*
10:	/SID88/gcgdata/geneseq/geneseq/AA1989.DAT:*
11:	/SID88/gcgdata/geneseq/geneseq/AA1990.DAT:*
12:	/SID88/gcgdata/geneseq/geneseq/AA1991.DAT:*
13:	/SID88/gcgdata/geneseq/geneseq/AA1992.DAT:*
14:	/SID88/gcgdata/geneseq/geneseq/AA1993.DAT:*
15:	/SID88/gcgdata/geneseq/geneseq/AA1994.DAT:*
16:	/SID88/gcgdata/geneseq/geneseq/AA1995.DAT:*
17:	/SID88/gcgdata/geneseq/geneseq/AA1996.DAT:*
18:	/SID88/gcgdata/geneseq/geneseq/AA1997.DAT:*
19:	/SID88/gcgdata/geneseq/geneseq/AA1998.DAT:*
20:	/SID88/gcgdata/geneseq/geneseq/AA1999.DAT:*
21:	/SID88/gcgdata/geneseq/geneseq/AA2000.DAT:*
22:	/SID88/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1809	100.0	340	21	AA15168	Rat Taste Cell spe
2	1806	99.8	340	21	AA15170	Mutant rat Taste C
3	1806	99.8	340	21	AA15171	Mutant rat Taste C
4	1805	99.8	340	21	AA15172	Mutant rat Taste C
5	1762	97.4	340	19	AAW3598	Human G protein be
6	1762	97.4	340	21	AA15169	Human Taste Cell s
7	1762	97.4	340	21	AA15173	Human Hgb3 G-prot
8	1760	97.3	340	21	AA15174	Mutant human Taste
9	1759	97.2	340	21	AA15175	Mutant human Taste
10	1759	97.2	340	21	AA15175	Mutant human Taste
11	1573	87.0	340	16	AA15168	WD-40 domain-contg

12	1573	87.0	340	21	AA15168	AA15168
13	1523	84.2	340	16	AA15168	AA15168
14	1523	84.2	340	21	AA15168	AA15168
15	1520.5	84.1	299	19	AAW59364	AAW59364
16	1518.5	83.9	297	21	AAW90939	AAW90939
17	1493	82.5	340	21	AA15168	AA15168
18	1467	81.1	341	16	AA15168	AA15168
19	1452	80.3	340	16	AA15168	AA15168
20	1419	78.4	326	16	AA15168	AA15168
21	945.5	52.3	395	20	AA15168	AA15168
22	945.5	52.3	353	21	AA15168	AA15168
23	901.5	49.8	371	21	AA15168	AA15168
24	863.5	47.7	295	22	AA15168	AA15168
25	860.5	47.6	295	22	AA15168	AA15168
26	817	45.2	377	21	AA15168	AA15168
27	655.5	36.2	229	22	AA15168	AA15168
28	652.5	36.1	267	21	AA15168	AA15168
29	652.5	36.1	267	21	AA15168	AA15168
30	639	35.3	423	20	AA15168	AA15168
31	639	35.3	423	16	AA15168	AA15168
32	639	35.3	423	21	AA15168	AA15168
33	638	35.3	422	20	AA15168	AA15168
34	635	35.1	423	21	AA15168	AA15168
35	635	35.1	423	21	AA15168	AA15168
36	609.5	32.8	225	22	AA15168	AA15168
37	593	32.8	243	21	AA15168	AA15168
38	571	31.6	166	21	AA15168	AA15168
39	528	29.2	227	21	AA15168	AA15168
40	528	29.2	227	21	AA15168	AA15168
41	421.5	23.3	203	21	AA15168	AA15168
42	308.5	17.1	485	22	AA15168	AA15168
43	308	17.0	333	21	AA15168	AA15168
44	299	16.5	471	21	AA15168	AA15168
45	299	16.5	471	21	AA15168	AA15168

ALIGNMENTS

RESULT	1
ID	AA15168 standard; Protein; 340 AA.
AC	AA15168;
XX	12-DEC-2000 (first entry)
DT	Rat Taste Cell specific G-protein beta 3 subunit.
XX	
DE	Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
XX	taste transduction pathway; pharmaceutical; food industry.
KW	
XX	
OS	Rattus sp.
XX	
PN	W0200045179-A2.
XX	
PD	03-AUG-2000.
XX	
PF	26-JAN-2000; 2000WO-US02218.
XX	
PR	27-JAN-1999; 99US-0117404.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Zuker CS, Adler JE, Lindemeier J;
XX	WPI; 2000-499361/44.
DR	N-PSDB; AAA74590.
XX	
PT	Identifying a compound that modulates sensory signaling in sensory
PT	cells for use in pharmaceutical and food industries comprises
PT	contacting the compound with a sensory cell specific G-protein beta
PT	polypeptide -

Human Hgb1 G-prot
WD-40 domain-contg
Human Hgb2 G-prot
Human G-protein be
Human G-protein be
Human G-protein be
Mouse Mgb4 G-prot
WD-40 domain-contg
WD-40 domain-contg
WD-40 domain-contg
Human cell cycle r
Human Mgb5 G-prot
Mouse pancreatic c
Human pancreatic c
Gene 45 human secr
Human secreted pro
Arabidopsis thalia
Gene 45 human secr
Arabidopsis thalia
Arabidopsis thalia
Yeast G protein be
WD-40 domain-contg
Ste4p/Gbeta intera
Yeast G protein be
Yeast G protein be
Yeast Ste4 protein
Human secreted pro
Breast and ovarian
Human cancer assoc
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Human GTP-binding
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia

XX Claim 1; Page 62; 68pp; English.
PS
CC The present sequence is rat G-protein beta 3 subunit. G-protein beta 3 is
CC expressed specifically in taste cells, hence this sequence is referred to
CC as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is
CC involved in the taste transduction pathway. TC-Gbeta3 may be used for
CC identifying taste modulating compounds which can be used in
CC pharmaceutical and food industries to customise taste.
XX
SQ Sequence 340 AA;

Query Match 100.0%; Score 1809; DB 21; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.2e-170;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMQLKQEAQOLKQIADARACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYA 60
Db 1 mgemqlkgeaeqlkqadarkacacditlaelvsglevgrvmtrtrtlrghlakiya 60
QY 61 MHWATDSKLLVASASQDGLIWDYTTTNKVAIPLRSSWVMTCAYAPSGNFVACGGLDNM 120
Db 61 mhwatdsklivsasqdgkllwtdytnkvhaiplrswvmtcayapsnfvacgglndm 120
QY 121 CSISYLSKREGNVKVSRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 180
Db 121 csisylksregnvkvsrelsahtgyiscrrfldnnivtssgdttcaldwletgqoktvf 180
QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
Db 181 vghtgdcmslavspdyklfiscgadksaklmdvregtcrotftghesdinaicfpngea 240
QY 241 ICTGSDASCRLFDLRADQELTAYSHESITGITSVAFSLSGRLLFAGYDDFNCNVWDSL 300
Db 241 ictgsddascrlfdlraddqeltayshesitcgitsvafslsgrllfagyddfncnvwds1 300
QY 301 KCERVGVLSGHDNRVSCIGVTADGMAVATGSWDSFLKIMN 340
Db 301 kcervgvlsghdnrvscigvtadgmavatsgwsdflikimn 340

RESULT 2
AAB15170
ID AAB15170 standard; Protein; 340 AA.
XX
AC AAB15170;
XX
DT 12-DEC-2000 (first entry)
XX
DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #1.
XX
KW Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
KW taste transduction pathway; pharmaceutical; food industry; mutation;
KW mutant; mutant.
XX
OS Rattus sp.
OS Synthetic.
XX
FH Key
FT Misc-difference 8 Location/Qualifiers
ET /note= "Wild-type Lys substituted by Arg"
XX
PN WO200045179-A2.
XX
PD 03-AUG-2000.
XX
PF 26-JAN-2000; 2000WO-US02218.
XX
PR 27-JAN-1999; 99US-0117404.
XX
PA (REGC) UNIV CALIFORNIA.
XX

PI Zuker CS, Adler JE, Lindemeyer J;
XX WPI; 2000-499361/44.
DR
XX
PT Identifying a compound that modulates sensory signaling in sensory
PT cells for use in pharmaceutical and food industries comprises
PT contacting the compound with a sensory cell specific G-protein beta
PT polypeptide -
XX
PS Disclosure; Page -; 68pp; English.
XX
CC The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
CC beta 3 is expressed specifically in taste cells, hence this sequence is
CC referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
CC be used for identifying taste modulating compounds which can be used in
CC pharmaceutical and food industries to customise taste.
CC Note: The present sequence is not shown in the specification but is
CC derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
CC AAB15168) and information given on page 8 of the disclosure.
XX
SQ Sequence 340 AA;

Query Match 99.8%; Score 1806; DB 21; Length 340;
Best Local Similarity 99.7%; Pred. No. 1e-169;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMQLKQEAQOLKQIADARACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYA 60
Db 1 mgemqlkgeaeqlkqadarkacacditlaelvsglevgrvmtrtrtlrghlakiya 60
QY 61 MHWATDSKLLVASASQDGLIWDYTTTNKVAIPLRSSWVMTCAYAPSGNFVACGGLDNM 120
Db 61 mhwatdsklivsasqdgkllwtdytnkvhaiplrswvmtcayapsnfvacgglndm 120
QY 121 CSISYLSKREGNVKVSRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 180
Db 121 csisylksregnvkvsrelsahtgyiscrrfldnnivtssgdttcaldwletgqoktvf 180
QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
Db 181 vghtgdcmslavspdyklfiscgadksaklmdvregtcrotftghesdinaicfpngea 240
QY 241 ICTGSDASCRLFDLRADQELTAYSHESITGITSVAFSLSGRLLFAGYDDFNCNVWDSL 300
Db 241 ictgsddascrlfdlraddqeltayshesitcgitsvafslsgrllfagyddfncnvwds1 300
QY 301 KCERVGVLSGHDNRVSCIGVTADGMAVATGSWDSFLKIMN 340
Db 301 kcervgvlsghdnrvscigvtadgmavatsgwsdflikimn 340

RESULT 3
AAB15171
ID AAB15171 standard; Protein; 340 AA.
XX
AC AAB15171;
XX
DT 12-DEC-2000 (first entry)
XX
DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #2.
XX
KW Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
KW taste transduction pathway; pharmaceutical; food industry; mutation;
KW mutant; mutant.
XX
OS Rattus sp.
OS Synthetic.
XX
FH Key
FT Misc-difference 12 Location/Qualifiers
ET /note= "Wild-type Glu substituted by Asp"
XX

XX WO200045179-A2.
 XX 03-AUG-2000.
 XX 26-JAN-2000; 2000WO-US02218.
 XX 27-JAN-1999; 99US-0117404.
 XX (REGC) UNIV CALIFORNIA.
 XX Zuker CS, Adler JE, Lindemeier J;
 XX WPI; 2000-499361/44.
 XX Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 XX
 XX Disclosure; Page -: 68pp; English.
 XX The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
 CC beta 3 is expressed specifically in taste cells, hence this sequence is
 CC referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
 CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
 CC be used for identifying taste modulating compounds which can be used in
 CC pharmaceutical and food industries to customise taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
 CC AAB15168) and information given on page 8 of the disclosure.
 XX
 XX Sequence 340 AA;
 SQ
 QY 1 MGEMEOLKQEAQOLKKQIADARKACADITLAEVSGLEVGRVQMRTRLRGLAKIYA 60
 Db 1 mgemeqlkgeadqlkkqiadarkacadiitlaelvsglevgrvqmrtrtlrghlaksiya 60
 QY 61 MHWATDSKLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 Db 61 mhwatdsklvssasqdgkliwtdtyttknvhairlrsswmtcayapsgnfvacggldnm 120
 QY 121 CSISYLSKREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQOKTVF 180
 Db 121 csisylksregnvkvsrelsahhtgylsccrflddnnivtssgdttcaldietgqoktvf 180
 QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQFTGHESDINAIICFPNGEA 240
 Db 181 vghtgdcmslavspdyklfisgacdasakimdvregtcrcqftghesdinaiicfpngea 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFSISGRLLFAGYDDFNCNVWDSL 300
 Db 241 ictgsddascrlfdlradeletayshesicgitsvafsisgrllfagyddfncnvwds1 300
 QY 301 KCERVGVLSGHDNRVSCLGVTADGMAVATGSDSFLKIWN 340
 Db 301 kcervgvlsghdnrvsclgvtadgmavatsgdsfllkiwn 340
 RESULT 4
 AAB15172
 ID AAB15172 standard; Protein; 340 AA.
 XX AAB15172;
 AC
 XX 12-DEC-2000 (first entry)
 DT
 XX Mutant rat Taste Cell specific G-protein beta 3 subunit variant #3.
 DE

XX Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 KW mutant;
 XX
 XX Rattus sp.
 OS Synthetic.
 OS
 XX
 FH Key location/Qualifiers
 FT Misc-difference 191 /note- "Wild-type Ala substituted by Gly"
 FT
 XX WO200045179-A2.
 XX 03-AUG-2000.
 XX 26-JAN-2000; 2000WO-US02218.
 XX 27-JAN-1999; 99US-0117404.
 XX (REGC) UNIV CALIFORNIA.
 XX Zuker CS, Adler JE, Lindemeier J;
 XX WPI; 2000-499361/44.
 XX Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 XX
 XX Disclosure; Page -: 68pp; English.
 XX The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
 CC beta 3 is expressed specifically in taste cells, hence this sequence is
 CC referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
 CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
 CC be used for identifying taste modulating compounds which can be used in
 CC pharmaceutical and food industries to customise taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
 CC AAB15168) and information given on page 8 of the disclosure.
 XX
 XX Sequence 340 AA;
 SQ
 QY 1 MGEMEOLKQEAQOLKKQIADARKACADITLAEVSGLEVGRVQMRTRLRGLAKIYA 60
 Db 1 mgemeqlkgeadqlkkqiadarkacadiitlaelvsglevgrvqmrtrtlrghlaksiya 60
 QY 61 MHWATDSKLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 Db 61 mhwatdsklvssasqdgkliwtdtyttknvhairlrsswmtcayapsgnfvacggldnm 120
 QY 121 CSISYLSKREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQOKTVF 180
 Db 121 csisylksregnvkvsrelsahhtgylsccrflddnnivtssgdttcaldietgqoktvf 180
 QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQFTGHESDINAIICFPNGEA 240
 Db 181 vghtgdcmslavspdyklfisgacdasakimdvregtcrcqftghesdinaiicfpngea 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFSISGRLLFAGYDDFNCNVWDSL 300
 Db 241 ictgsddascrlfdlradeletayshesicgitsvafsisgrllfagyddfncnvwds1 300
 QY 301 KCERVGVLSGHDNRVSCLGVTADGMAVATGSDSFLKIWN 340
 Db 301 kcervgvlsghdnrvsclgvtadgmavatsgdsfllkiwn 340

RESULT 5

AAW36598

ID AAW36598 standard; Protein; 340 AA.

XX AC AAW36598;

DT 19-MAY-1998 (first entry)

DE Human G protein beta-3 subunit.

KW G protein beta-3 subunit; variant; mutation; hypertension; diagnosis;
cardiovascular disease; metabolic disorder; immunological disorder.

OS Homo sapiens.

PN DE19619362-A1.

PD 20-NOV-1997.

PF 14-MAY-1996; 96DE-1019362.

PR 14-MAY-1996; 96DE-1019362.

PA (BADI) BASF AG.

PI Siffert W;

DR WPI; 1998-000675/01.

DR N-PSDB; AAT96746; AAV09741.

PT Assessing risk of disease, especially hypertension - by detecting
mutation in human G-protein beta-3 subunit gene

PS Claim 3; Page 6; 8pp; German.

CC This sequence represents the human G-protein beta 3 subunit. A variant
of the gene encoding this protein has applications in the diagnosis of
diseases or assessing the risk of a disease associated with G-protein
misregulation. G-protein misregulation is associated with hypertension,
cardiovascular diseases e.g. coronary heart disease, atherosclerosis,
restenosis, stroke and thrombosis, metabolic disorders such as diabetes,
diabetic complications, disorders of lipid metabolism and central
chemoreception dysfunction (e.g. sudden infant death syndrome), and
immunological disorders such as impaired wound healing, tumours, AIDS,
cirrhosis and transplant rejection.

CC Sequence 340 AA;

Query Match

Best Local Similarity 97.4%; Score 1762; DB 19; Length 340;

Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEOLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60

DB 1 mgemeqlrgeaeqlkkqladarkacadvtlaelvsglevgrvqmrtrrlrghlakiya 60

QY 61 MHMATDSKLVASASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120

DB 61 mhmatdsklvassasqdgkllwdsyttnkvhaiprrsswmtcayapsgnfvacgglndm 120

QY 121 CSITSLSREGNVKVSRELSTHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGOQKTVF 180

DB 121 csitlsksregnvkvsrelsthtgylsccrflddnnivtssgdttcaldietgqktvf 180

QY 181 VGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHSNDINAICFPNGEA 240

DB 181 vghgtgdcmslavspdyklfiscgadasklmdvregtcrcftghesndinaicfpngea 240

QY 241 ICTGSDDASCRLFLRADQELTAYSHESITICITSVAFSLSGRLLFAGYDDFNQNVWDSL 300

DB 241 ictgsddascrlfldradqelctayshesitictitsvafslsgrllfagyddfnqnvwdsl 300

DB 241 ictgsddascrlfldradqelctayshesitictitsvafslsgrllfagyddfnqnvwdsl 300

QY 301 KCERVGVLSGHDNRVSCIGVTADGMAYATGSMDFLKIWN 340

DB 301 kservglsghdnrvscigvtadgmavatsgswdflikwn 340

RESULT 6

AAB15169

ID AAB15169 standard; Protein; 340 AA.

XX AC AAB15169;

DT 12-DEC-2000 (first entry)

DE Human Taste Cell specific G-protein beta 3 subunit.

KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
taste transduction pathway; pharmaceutical; food industry.

OS Homo sapiens.

PN WO200045179-A2.

PD 03-AUG-2000.

PF 26-JAN-2000; 2000WO-US02218.

PR 27-JAN-1999; 99US-0117404.

PA (REGC) UNIV CALIFORNIA.

PI Zuker CS, Adler JE, Lindemeier J;

DR WPI; 2000-499361/44.

DR N-PSDB; AAA74591.

PT Identifying a compound that modulates sensory signaling in sensory
cells for use in pharmaceutical and food industries comprises
contacting the compound with a sensory cell specific G-protein beta
polypeptide -

PS Claim 1; Page 63; 68pp; English.

CC The present sequence is human G-protein beta 3 subunit. G-protein beta 3
is expressed specifically in taste cells, hence this sequence is referred
to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3
is involved in the taste transduction pathway. TC-Gbeta3 may be used for
identifying taste modulating compounds which can be used in
pharmaceutical and food industries to customise taste.

CC Sequence 340 AA;

Query Match

Best Local Similarity 97.4%; Score 1762; DB 21; Length 340;

Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEOLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60

DB 1 mgemeqlrgeaeqlkkqladarkacadvtlaelvsglevgrvqmrtrrlrghlakiya 60

QY 61 MHMATDSKLVASASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120

DB 61 mhmatdsklvassasqdgkllwdsyttnkvhaiprrsswmtcayapsgnfvacgglndm 120

QY 121 CSITSLSREGNVKVSRELSTHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGOQKTVF 180

DB 121 csitlsksregnvkvsrelsthtgylsccrflddnnivtssgdttcaldietgqktvf 180

QY 181 VGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHSNDINAICFPNGEA 240

DB 181 vghgtgdcmslavspdyklfiscgadasklmdvregtcrcftghesndinaicfpngea 240

QY 241 ICTGSDDASCRLFDLRADQELTAYSHESIICGITSVAFLSGRLLFAGYDDFNCNWDSL 300
 Db 241 ictgsddascrlfdlradqelictshesilcgitvafslsgrllfagyddfncnwds 300
 QY 301 KCERVGVLGHDNRVSCIGVTADGMAVATGSDSFLKIWN 340
 Db 301 kservgilsghdnrsvclgytadgmavatsgwsdflikwn 340

RESULT 7
 AAY67865
 ID AAY67865 standard; protein; 340 AA.
 AC AAY67865;
 DT 25-APR-2000 (first entry)

DE Human Hgb3 G-protein beta3 subunit amino acid sequence.
 KW Ste20p/PAK; G-protein-coupled receptor signal transduction; human; Hgb3;
 KW Ste4p/Gbeta interaction domain; p21-activated protein kinase;
 KW G-protein coupled receptor signal transduction;
 OS Homo sapiens.
 PN CA2219958-A1.
 PD 07-JUL-1999.
 PF 07-JAN-1998; 98CA-2219958.
 PR 07-JAN-1998; 98CA-2219958.

PA (LEBEU/) LEBERER E.
 PA (LEEU/) LEEUW T.
 PA (THOM/) THOMAS D Y.
 PA (WHIT/) WHITEWAY M.
 PI Leberer E, Leeuw T, Thomas DY, Whiteaway M;

DR WPI; 2000-137553/13.
 XX Interacting polypeptides involved in G-protein-coupled receptor signal
 PT transduction -
 PS Claim 3; Fig 6; 91pp; English.

XX This sequence represents the beta3 subunit of a human G-protein. The
 CC invention relates to the G-protein beta subunit interaction domain of the
 CC Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein
 CC kinases are p21-activated protein kinases (PAK), and they are involved in
 CC many varied cellular processes ranging from morphogenesis and stress
 CC response, to apoptosis. Interacting polypeptides Ste4p/Gbeta and
 CC Ste20p/PAK are useful for designing in vitro and in vivo experimental
 CC models which enable the screening of large collections of synthetic,
 CC semi-synthetic, or natural compounds for therapeutic use in Ste4p/Gbeta
 CC and Ste20p/PAK dependent diseases.

XX Sequence 340 AA;
 SQ
 Query Match 97.4%; Score 1762; DB 21; Length 340;
 Best Local Similarity 96.5%; Pred. No. 2,3e-165;
 Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEQLKQEAQDLKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
 Db 1 mgemeqlrgeaeqlkqiadarkacadvltlaelvsglevgrvqmrtrrlrghlakiya 60
 QY 61 MHMATDSKLLVSASQDGLIWMDFYTTNKVHAIPLRSSWVMTCAVAPSGNFVACGLDNM 120
 Db 61 mhmatdskllvsasqdgklliwmdsyttnkvhaiplrswmtcayapsngnfvacgldnm 120

QY 121 CSIYSLKREGNVKVSRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGOOKTVE 180
 Db 121 csiynlksregnvksrelsahtgylsccrflddnnivtssgdttcaldietgqktvf 180
 QY 181 VGHGDCMSLAVSPDYKFLFISGACDASAKLMDVREGTCRQFTGHESDINACEFPNGEA 240
 Db 181 vghtgcdmslavspdynflfisgacdasaklmdvregtcrtqftghesdinacifpngea 240
 QY 241 ICTGSDDASCRLFDLRADQELTAYSHESIICGITSVAFLSGRLLFAGYDDFNCNWDSL 300
 Db 241 ictgsddascrlfdlradqelictshesilcgitvafslsgrllfagyddfncnwds 300
 QY 301 KCERVGVLGHDNRVSCIGVTADGMAVATGSDSFLKIWN 340
 Db 301 kservgilsghdnrsvclgytadgmavatsgwsdflikwn 340

RESULT 8
 AAB15173
 ID AAB15173 standard; protein; 340 AA.
 AC AAB15173;
 DT 12-DEC-2000 (first entry)

DE Mutant human Taste Cell specific G-protein beta 3 subunit variant #1.
 KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 KW mutein; mutant.
 OS Homo sapiens.
 OS Synthetic.

XX Key location/qualifiers
 FH Misc-difference 7 /note= "Wild-type Leu substituted by Ile"
 FT WO200045179-A2.
 PN 03-AUG-2000.
 PD 26-JAN-2000; 2000WO-US02218.
 PF 27-JAN-1999; 99US-0117404.
 PR (REGC) UNIV CALIFORNIA.
 PA Zuker CS, Adler JE, Lindemeier J;

PI WPI; 2000-499361/44.
 XX Identifying a compound that modulates sensory signaling in sensory
 CC cells for use in pharmaceutical and food industries comprises
 CC contacting the compound with a sensory cell specific G-protein beta
 CC polypeptide -
 PS Disclosure; page -; 68pp; English.

XX The present sequence is a mutant human G-protein beta 3 subunit. this
 CC G-protein beta 3 is expressed specifically in taste cells, hence this
 CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
 CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
 CC TC-Gbeta3 may be used for identifying taste modulating compounds which
 CC can be used in pharmaceutical and food industries to customise taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type TC-Gbeta3 sequence given on page 63
 CC (see AAB15169) and information given on page 8 of the disclosure.

XX Sequence 340 AA;
 SQ

Query Match
Best Local Similarity 97.3%; Score 1760; DB 21; Length 340;
Matches 327; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEQLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYA 60
Db 1 mgemeqlrgeaeqlkkqiadaracadvlaelvsqlevgrvqmrtrtlrghlakiya 60
QY 61 MHWATDSKLVASASQDGKLIWDTYTNKVAIPLRSSWVMTCAAPSGNFVACGGLDNM 120
Db 61 mhwatdsklvassqdgkliwdsytlnkvaipirsswmtcayapsnfvacgglndm 120
QY 121 CSIYSLKSRREGNVKVSRELTAHTGYLSGCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 180
Db 121 cslynksregnvkvsrelsahhtgylscrrfddnnivtssgdttcaldwletgqktvf 180
QY 181 VGHGTDCMSLAVSPDYKLEIFSGACDASAKLMDVREGTCRQFTTGHESDINAIKCFPNGEA 240
Db 181 vghtgdcmslavspdykelfisgacdasaklmdvregtcrcrfttghesdinaicfpngea 240
QY 241 ICTGSDDASCRLFDLRADQELTAYSHESIICGITSVAFSLGRLPAGYDDFNCNVWDSL 300
Db 241 ictgsddascrlfdlradqelictshesilcgitsvafslsgrllfagyddfncnvwds 300
QY 301 KCERVGVLSGHDNRVSCIGVTADGMAVATGSWDSFLKIWN 340
Db 301 kservglisghdnrvsclygtadgmavatswdsflkiwn 340

RESULT 9
AAB15174
ID AAB15174 standard; Protein; 340 AA.
AC AAB15174;
DT 12-DEC-2000 (first entry)
DE Mutant human Taste Cell specific G-protein beta 3 subunit variant #2.
KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
KW taste transduction pathway; pharmaceutical; food industry; mutation;
XX mutant.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 161 /note- "Wild-type Ser substituted by Thr"
FT
XX
XX
PN WO200045179-A2.
XX
PD 03-AUG-2000.
XX
XX
PF 26-JAN-2000; 2000WO-US02218.
XX
XX
PR 27-JAN-1999; 99US-0117404.
XX
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Zuker CS, Adler JE, Lindemeier J;
XX
DR WPI; 2000-499361/44.
XX
XX
PT Identifying a compound that modulates sensory signaling in sensory
PT cells for use in pharmaceutical and food industries comprises
PT contacting the compound with a sensory cell specific G-protein beta
PT polypeptide -
XX
XX
PS Disclosure; Page -; 68pp; English.
XX
XX
CC The present sequence is a mutant human G-protein beta 3 subunit.
CC G-protein beta 3 is expressed specifically in taste cells, hence this

CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
CC TC-Gbeta3 may be used for identifying taste modulating compounds which
CC can be used in pharmaceutical and food industries to customise taste.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type TC-Gbeta3 sequence given on page 63
CC (see AAB15169) and information given on page 8 of the disclosure.
XX
SQ Sequence 340 AA;

Query Match
Best Local Similarity 97.2%; Score 1759; DB 21; Length 340;
Matches 327; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEQLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYA 60
Db 1 mgemeqlrgeaeqlkkqiadaracadvlaelvsqlevgrvqmrtrtlrghlakiya 60
QY 61 MHWATDSKLVASASQDGKLIWDTYTNKVAIPLRSSWVMTCAAPSGNFVACGGLDNM 120
Db 61 mhwatdsklvassqdgkliwdsytlnkvaipirsswmtcayapsnfvacgglndm 120
QY 121 CSIYSLKSRREGNVKVSRELTAHTGYLSGCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 180
Db 121 cslynksregnvkvsrelsahhtgylscrrfddnnivtssgdttcaldwletgqktvf 180
QY 181 VGHGTDCMSLAVSPDYKLEIFSGACDASAKLMDVREGTCRQFTTGHESDINAIKCFPNGEA 240
Db 181 vghtgdcmslavspdykelfisgacdasaklmdvregtcrcrfttghesdinaicfpngea 240
QY 241 ICTGSDDASCRLFDLRADQELTAYSHESIICGITSVAFSLGRLPAGYDDFNCNVWDSL 300
Db 241 ictgsddascrlfdlradqelictshesilcgitsvafslsgrllfagyddfncnvwds 300
QY 301 KCERVGVLSGHDNRVSCIGVTADGMAVATGSWDSFLKIWN 340
Db 301 kservglisghdnrvsclygtadgmavatswdsflkiwn 340

RESULT 10
AAB15175
ID AAB15175 standard; Protein; 340 AA.
AC AAB15175;
DT 12-DEC-2000 (first entry)
DE Mutant human Taste Cell specific G-protein beta 3 subunit variant #3.
KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
KW taste transduction pathway; pharmaceutical; food industry; mutation;
XX mutant.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 301 /note- "Wild-type Lys substituted by Arg"
FT
XX
XX
PN WO200045179-A2.
XX
PD 03-AUG-2000.
XX
XX
PF 26-JAN-2000; 2000WO-US02218.
XX
XX
PR 27-JAN-1999; 99US-0117404.
XX
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Zuker CS, Adler JE, Lindemeier J;
XX

DR WPI; 2000-499361/44.

XX Identifying a compound that modulates sensory signaling in sensory
PT cells for use in pharmaceutical and food industries comprises
PT contacting the compound with a sensory cell specific G-protein beta
PT polypeptide -

XX
PS Disclosure; Page -: 66pp; English.

CC The present sequence is a mutant human G-protein beta 3 subunit.
CC G-protein beta 3 is expressed specifically in taste cells, hence this
CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
CC TC-Gbeta3 may be used for identifying taste modulating compounds which
CC can be used in pharmaceutical and food industries to customise taste.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type TC-Gbeta3 sequence given on page 63
CC (see AAB15169) and information given on page 8 of the disclosure.

XX
SQ Sequence 340 AA;

Query Match 97.2%; Score 1759; DB 21; Length 340;
Best Local Similarity 96.2%; Pred. No. 4.4e-165;
Matches 327; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

OY 1 MGEMEQLKQEAQKQIADARKACADITLAEVSGLEVGRVQMRTRTRLRGLAKIYA 60
DB 1 mgemeqlrgeaeqlkqadarkacadvltlaelvsglevgrvqmrtrtrlrghlakiya 60

OY 61 MHWATDSKLVASQDGKLIWDTYTNKVHAIPLRSSWMTCAIAPSGNFVACGGLDNM 120
DB 61 mhwatdsklvsasdgkcliwdtytnkvhaiplrswmtcaiapsgnfvacgglndm 120

OY 121 CSIYSLKSREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQQTVE 180
DB 121 csiynlksregnvkvsrelsahthgylsccrflddnnivtssgdttcaldietgqqtvf 180

OY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICTFPNGEA 240
DB 181 vghgdcmslavspdyklfistgacdasaaklmdvregtcrtqftghesdinalctfngnea 240

OY 241 ICTGSDDASCRLFDLRADQELTAYSHESITCGITSVAFSLSGRLLFAGYDDFNCNVWDSL 300
DB 241 ictgsddascrlfdlradeqelictshesitcgitsvafslsgrllfagyddfncnvwsl 300

OY 301 KCERVGVLSGHDNRVSCIGVTADGMAVATGSWDSFLKIWN 340
DB 301 kservgvlsghdnrvscigtadtgmavatswdsflkiwn 340

RESULT 11
AAR85859
ID AAR85859 standard; peptide; 340 AA.

XX
AC AAR85859;
XX
DT 13-SEP-1996 (first entry)
XX
DE WD-40 domain-contg. bovine G-beta-1 protein.
XX
KW WD40 repeat region; beta-transducin; protein-protein interaction; drug;
KW intracellular signaling; protein kinase C; homology; motif; modulator;
KW receptors of activated protein kinase; enzyme activity; isozyme; human.
XX
OS Bos taurus.
XX
PN WO9521252-A2.
XX
PD 10-AUG-1995.
XX
PF 31-JAN-1995; 95WO-US01210.
XX

PR 01-FEB-1994; 94US-0190802.

XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Mochly-Rosen D, Ron D;
XX
DR WPI; 1995-283772/37.

XX
XX New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
PT activity of a protein, eg. protein kinase C, which interacts with a
PT protein contg. a WD-40 region.

XX
PS Example 5; Page 102-103; 351pp; English.

CC Proteins AAR85851-92 are protein which contain at least one WD-40 (also
CC called beta-transducing homologous) amino acid repeat motifs. The WD-40
CC regions are involved in protein-protein interactions between proteins
CC involved in intracellular signalling. An example of such an interaction
CC is between protein kinase C and receptors of activated protein kinase
CC (RACK), esp. RACK-1 (AAR85850). Proteins AAR85851-82 were isolated based
CC on homology with beta-transducin, whereas proteins AAR85882-92 were
CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
CC The proteins were used to construct the peptides AAR84928-R85063 and
CC AAR85786-R85842. The peptides can be used to identify target proteins
CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
CC proteins involved in protein-protein interaction and to screen for drugs
CC that will affect protein-protein interaction involving WD-40 domains.

XX
SQ Sequence 340 AA;

Query Match 87.0%; Score 1573; DB 16; Length 340;
Best Local Similarity 83.2%; Pred. No. 9.6e-147;
Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

OY 1 MGEMEQLKQEAQKQIADARKACADITLAEVSGLEVGRVQMRTRTRLRGLAKIYA 60
DB 1 mseldqlrgeaeqlknqirdarkacadatlsqitnldpygrlqmrtrtrlrghlakiya 60

OY 61 MHWATDSKLVASQDGKLIWDTYTNKVHAIPLRSSWMTCAIAPSGNFVACGGLDNM 120
DB 61 mhwtidsrlivsasdgkcliwdtytnkvhaiplrswmtcaiapsgnyvacgglndi 120

OY 121 CSIYSLKSREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQQTVE 180
DB 121 csiynlksregnvkvsrelsahthgylsccrflddnnivtssgdttcaldietgqqtvf 180

OY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICTFPNGEA 240
DB 181 tghtgdvmslavadtrllfvsagcdasaaklmdvregmcrqftghesdinalctfngnea 240

OY 241 ICTGSDDASCRLFDLRADQELTAYSHESITCGITSVAFSLSGRLLFAGYDDFNCNVWDSL 300
DB 241 fatgsddatcrlfdlradeqelictshesitcgitsvafslsgrllfagyddfncnvwsl 300

OY 301 KCERVGVLSGHDNRVSCIGVTADGMAVATGSWDSFLKIWN 340
DB 301 kdragvlaghdnrvscigtadtgmavatswdsflkiwn 340

RESULT 12
AAY67863
ID AAY67863 standard; protein; 340 AA.

XX
AC AAY67863;
XX
DT 25-APR-2000 (first entry)
XX
DE Human Hgb1 G-protein betal subunit amino acid sequence.
XX
KW Ste20p/PAK; G-protein-coupled receptor signal transduction; human; Hgb1;
KW Ste4p/Gbeta interaction domain; p21-activated protein kinase;
KW G-protein coupled receptor signal transduction;
KW

XX Homo sapiens.
 OS
 XX
 PN CA2219958-A1.
 XX
 PD 07-JUL-1999.
 XX
 PF 07-JAN-1998; 98CA-2219958.
 XX
 PR 07-JAN-1998; 98CA-2219958.
 XX
 PA (LEBEU/) LEBERER E.
 PA (LEEU/) LEEUW T.
 PA (THOM/) THOMAS D Y.
 PA (WHIT/) WHITEWAY M.
 XX
 PI Leberer E, Leeuw T, Thomas DY, Whiteway M;
 XX
 DR WPI; 2000-137553/13.
 XX
 PT Interacting polypeptides involved in G-protein-coupled receptor signal
 PT transduction -
 XX
 PS Claim 3; Fig 6; 91pp; English.
 XX
 CC This sequence represents the beta1 subunit of a human G-protein. The
 CC invention relates to the G-protein beta subunit interaction domain of the
 CC Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein
 CC kinases are p21-activated protein kinases (PAK), and they are involved in
 CC many varied cellular processes ranging from morphogenesis and stress
 CC response, to apoptosis. Interacting polypeptides Ste4p/Gbeta and
 CC Ste20p/PAK are useful for designing in vitro and in vivo experimental
 CC models which enable the screening of large collections of synthetic,
 CC semi-synthetic, or natural compounds for therapeutic use in Ste4p/Gbeta
 CC and Ste20p/PAK dependent diseases.
 XX
 SQ Sequence 340 AA;

Query Match 87.0%; Score 1573; DB 21; Length 340;
 Best Local Similarity 83.2%; Pred. No. 9.6e-147;
 Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;
 QY 1 MGEMEQLKQEAQLKKQIADARKACADITLAEVLVSGLEVGRVQMRTRTLRGLAKIYA 60
 Db 1 mseldqlrgeaeqlknqirdarkacadatlsqitnldpvgriqmrtrtlrghlakiya 60
 QY 61 MHMATDSKLVASASQDGKLIWDTYTNKVHAIPLRSSWVMTCAVAPSGNFVACGGLDNM 120
 Db 61 mhwtgdsrlivsasqdgkllwdsyttnkvhaiprrsswmtcayapsngnvacgldnl 120
 QY 121 CSISYLSKREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQOKTVF 180
 Db 121 cslynlktregnvrvsrelaghtyysccrflldnnivtssgdtlcalwdietgqttf 180
 QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
 Db 181 tghtgdvmslslapdtrlfvsgacdasaklwdvregmcrqftghesdinaicfpngna 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFSLSGRLLFAGYDDFNCNWWSL 300
 Db 241 fatgsddatcrlfdlradqelmyshdnlicgitsvafslsgsgrlllagyddfnncnwda 300
 QY 301 KCERVGVLSGHDNRVSCLGVTADGMAVATGSWDSFLKIWN 340
 Db 301 kdragvylaghdnrsvclgvtadgmavatsgswdsflkiwn 340

RESULT 13
 AAR85863
 ID AAR85863 standard; peptide; 340 AA.
 XX
 AC AAR85863;

XX 13-SEP-1996 (first entry)
 DT
 XX
 DE WD-40 domain-contg. human G-beta-2 protein.
 XX
 KW WD40 repeat region; beta-transducin; protein-protein interaction; drug;
 KW intracellular signalling; protein kinase C; homology; motif; modulator;
 KW receptors of activated protein kinase; enzyme activity; isozyme; human.
 XX
 OS Homo sapiens.
 XX
 PN W09521252-A2.
 XX
 PD 10-AUG-1995.
 XX
 PF 31-JAN-1995; 95WO-US01210.
 XX
 PR 01-FEB-1994; 94US-0190802.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Mochly-Rosen D, Ron D;
 XX
 DR WPI; 1995-283772/37.
 XX
 PT New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
 PT activity of a protein, eg. protein kinase C, which interacts with a
 PT protein contg. a WD-40 region.
 XX
 PS Example 5; Page 109-110; 351pp; English.
 XX
 CC Proteins AAR85851-92 are protein which contain at least one WD-40 (also
 CC called beta-transducin homologous) amino acid repeat motifs. The WD-40
 CC regions are involved in protein-protein interactions between proteins
 CC involved in intracellular signalling. An example of such an interaction
 CC is between protein kinase C and receptors of activated protein kinase
 CC (RACK), esp. RACK-1 (AAR85850). Proteins AAR85851-82 were isolated based
 CC on homology with beta-transducin, whereas proteins AAR85882-92 were
 CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
 CC The proteins were used to construct the peptides AAR84928-R85063 and
 CC AAR85786-R85842. The peptides can be used to identify target proteins
 CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
 CC proteins involved in protein-protein interaction and to screen for drugs
 CC that will affect protein-protein interaction involving WD-40 domains.
 XX
 SQ Sequence 340 AA;

Query Match 84.2%; Score 1523; DB 16; Length 340;
 Best Local Similarity 80.9%; Pred. No. 8.1e-142;
 Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;
 QY 1 MGEMEQLKQEAQLKKQIADARKACADITLAEVLVSGLEVGRVQMRTRTLRGLAKIYA 60
 Db 1 mselqlrgeaeqlknqirdarkacagdstltqtagldpvgriqmrtrtlrghlakiya 60
 QY 61 MHMATDSKLVASASQDGKLIWDTYTNKVHAIPLRSSWVMTCAVAPSGNFVACGGLDNM 120
 Db 61 mhwtgdsrlivsasqdgkllwdsyttnkvhaiprrsswmtcayapsngnvacgldnl 120
 QY 121 CSISYLSKREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQOKTVF 180
 Db 121 cslynlktregnvrvsrelpghtyysccrflldnnivtssgdtlcalwdietgqtvf 180
 QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
 Db 181 aghsgdvmslslapdtrlfvsgacdasaklwdvrdsmcrqftghesdinavafpngya 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFSLSGRLLFAGYDDFNCNWWSL 300
 Db 241 ftgsddatcrlfdlradqelmyshdnlicgitsvafslsgsgrlllagyddfnncnwdam 300
 QY 301 KCERVGVLSGHDNRVSCLGVTADGMAVATGSWDSFLKIWN 340

Db 301 kgdragvlaghndrvsclygtddgmavatgswdflikwn 340

RESULT 14

ID AAY67864 standard; protein; 340 AA.

AC AAY67864;

DT 25-APR-2000 (first entry)

DE Human Hgb2 G-protein beta2 subunit amino acid sequence.

KW Ste20p/PAK; G-protein-coupled receptor signal transduction; human; Hgb2;
KW Ste4p/Gbeta interaction domain; p21-activated protein kinase;
KW G-protein coupled receptor signal transduction;

OS Homo sapiens.

PN CA2219958-A1.

PD 07-JUL-1999.

PF 07-JAN-1998; 98CA-2219958.

PR 07-JAN-1998; 98CA-2219958.

PA (LEBE/) LEBERER E.

PA (LEEU/) LEEUW T.

PA (THOM/) THOMAS D Y.

PA (WHIT/) WHITEWAY M.

PI Leberer E, Leeuw T, Thomas DY, Whiteaway M;

DR WPI; 2000-137553/13.

PT Interacting polypeptides involved in G-protein-coupled receptor signal
transduction -

PS Claim 3; Fig 6; 91pp; English.

CC This sequence represents the beta2 subunit of a human G-protein. The
CC invention relates to the G-protein beta subunit interaction domain of the
CC Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein
CC kinases are p21-activated protein kinases (PAK), and they are involved in
CC many varied cellular processes ranging from morphogenesis and stress
CC response, to apoptosis. Interacting polypeptides Ste4p/Gbeta and
CC Ste20p/PAK are useful for designing in vitro and in vivo experimental
CC models which enable the screening of large collections of synthetic,
CC semi-synthetic, or natural compounds for therapeutic use in Ste4p/Gbeta
CC and Ste20p/PAK dependent diseases.

XX Sequence 340 AA;

QY Query Match 84.2%; Score 1523; DB 21; Length 340;
Best Local Similarity 80.9%; Pred. No. 8.1e-142;
Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

Db 1 MGEMEQLKQAEOLKQIADARKACADITLAEVLVSGLEVNGRVQMRTRRLRGHLAKIYA 60
1 mseqqlrgeaeqlngirdarkacagdstiltgtagldpvgriqmrtrrlrghlakiya 60

QY 61 MHWATDSKLLVASQDGLIWMVTYTNKVHAIPLRSSWVMTCAYAPSGNFVACGGIDNM 120
61 mhwtgdsrllvasasqdgkllwdsytnkvhaiprrsswvmtcayapsnfvacggidnm 120

Db 121 CSIYSLKSRGNVKSRELSAHTGILSCRFLLDNNITVSSGDTTCALWIDETGQKTVF 180
121 cslyslktrgnvksrelsahtgilsccrflldnnitvssgdttcawidietgqktvf 180

QY 181 VGHTGDCMSLAVSPDYKLFISGACDASAKLWMDVREGTCRQTFTHESDINACFFPNGEA 240
181 vghtgdcmslavspdyklfisgacdasaaklwmvdvregtcrqtfthesdinacffpnga 240

Db 181 aghsqdvmslsiapdgrtfvsgacdasiklwdvrdsmcrgtfighesdinavafpnyga 240

QY 241 ICTGSDASCRLFDLRADQELTAISHESIICGITSVAFSLSGRLLFAGYDDFNQNWDSL 300

Db 241 ftgsddatcrlfdlradqellmyshdnligitsvafsrgrlllagyddfnncniwdam 300

QY 301 KCERVGLSGHDNRVSCGLVTLADGMAVATGSDSFLKIMN 340

Db 301 kgdragvlaghndrvsclygtddgmavatgswdflikwn 340

RESULT 15

AAM59364

ID AAM59364 standard; Protein; 299 AA.

AC AAM59364;

DT 10-SEP-1998 (first entry)

DE Human G-protein beta-3 subunit protein.

KW G protein; beta-3 subunit; human; hypertension; immunodeficient; stroke;
KW treatment; cardiovascular disease; metabolic disorder; tumour metastasis;
KW coronary heart disease; post-angioplastic re-stenosis; diabetes;
KW nephropathy; polyneuropathy; retinopathy.

OS Homo sapiens.

PN WO9811212-A1.

PD 19-MAR-1998.

PF 29-AUG-1997; 97WO-EP04709.

PR 13-SEP-1996; 96DE-1037518.

PA (SIF/) SIFFERT W.

PI Siffert W;

DR WPI; 1998-271665/24.

PT Variant of human G protein beta-3 sub-unit - associated with
hypertension

PS Claim 2; Page 12-13; 34pp; German.

CC This sequence represents a human G-protein beta-3 subunit consisting
CC of up to six WD repeat motifs (as found in hypertensive subjects, rather
CC than the seven WD repeat motifs found in normotensive subjects). The
CC nucleic acid sequence encoding this protein can be expressed in a host
CC organism to produce the protein, preferably where the host organism is an
CC immunodeficient person, especially an HIV-positive person. This sequence
CC can be used to prepare a medicament for treating diseases associated with
CC G protein mis-control e.g. cardiovascular disease, metabolic disorders or
CC immunological diseases, hypertension, coronary heart disease, stroke,
CC post-angioplastic re-stenosis, diabetic complications (e.g. nephropathy,
CC polyneuropathy or retinopathy) or tumour metastasis.

XX Sequence 299 AA;

QY Query Match 84.1%; Score 1520.5; DB 19; Length 299;
Best Local Similarity 85.0%; Pred. No. 1.2e-141;
Matches 289; Conservative 7; Mismatches 3; Indels 41; Gaps 1;

Db 1 MGEMEQLKQAEOLKQIADARKACADITLAEVLVSGLEVNGRVQMRTRRLRGHLAKIYA 60
1 mgemeqlrgeaeqlkqiadarkacadvllaevlvsglevngvqmrtrrlrghlakiya 60

QY 61 MHWATDSKLLVASQDGLIWMVTYTNKVHAIPLRSSWVMTCAYAPSGNFVACGGIDNM 120
61 mhwtgdsrllvasasqdgkllwdsytnkvhaiprrsswvmtcayapsnfvacggidnm 120

Fri Sep 28 10:45:04 2001

us-09-492-029-3.rag

Page 10

```
Db      61 mhwatdskllvsasqdgkllvwdsytnkvhaiplrsswvmtcayapsgnfvacgldnm 120
QY      121 CSITSLKSRREGNVKVSRELSAHTGYLSCCRFLDDNNIYTSSGDTTCALMDIETGQOKTVF 180
Db      121 cslynlskregnvkvsrelsahgtysccrflddnniyltssgdttc----- 166
QY      181 VGHTEGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQTFTHESDINAIQCFPNGEA 240
Db      167 -----aklwdvregtcrgltfghesdinaicffpngea 199
QY      241 ICTGSDDASCRLFDLRADQELTAYSHESITCGITSVAFSLSGRLLFAGYDDFNCNVWDSL 300
Db      200 ictgsddascrlfdlradqelictfshesitcgitsvafsisgrllfagyddfnvwdsm 259
QY      301 KCERVGVLSGHDNRVSCIGVTADGMAVATGSWDSFLKIWN 340
Db      260 kservgvlsghdnrsvscigvtadgmavatgswdsflkiwn 299
```

Search completed: September 28, 2001, 10:29:21
Job time: 71 sec

Fri Sep 28 10:45:05 2001

us-09-492-029-3.ra1

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:28:09 ; Search time 20.71 Seconds
(without alignments)
338.036 Million cell updates/sec

Title: US-09-492-029-3
Perfect score: 1809
Sequence: 1 MGEMEQLKQAEQKQIAD.....TADGNAVATGSDSFLKIWN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 segs, 20590346 residues 197339

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1762	97.4	340	4	US-09-180-783-2	Sequence 2, Appli
2	1573	87.0	340	1	US-08-190-802A-38	Sequence 38, Appli
3	1523	84.2	340	1	US-08-190-802A-42	Sequence 42, Appli
4	1520.5	84.1	299	4	US-09-147-826B-2	Sequence 2, Appli
5	1467	81.1	341	1	US-08-190-802A-45	Sequence 45, Appli
6	1452	80.3	340	1	US-08-190-802A-40	Sequence 40, Appli
7	1419	78.4	326	1	US-08-190-802A-39	Sequence 39, Appli
8	946.5	52.3	395	3	US-09-032-372-1	Sequence 1, Appli
9	639	35.3	423	1	US-08-190-802A-61	Sequence 61, Appli
10	297.5	16.4	317	1	US-08-190-802A-27	Sequence 27, Appli
11	297.5	16.4	317	1	US-08-190-802A-41	Sequence 41, Appli
12	297.5	16.4	317	1	US-08-190-802A-47	Sequence 47, Appli
13	295	16.3	704	1	US-08-190-802A-62	Sequence 62, Appli
14	295	16.3	704	1	US-08-188-582-5	Sequence 5, Appli
15	295	16.3	704	1	US-08-646-715-5	Sequence 6, Appli
16	295	16.3	704	1	US-08-308-818-3	Sequence 3, Appli
17	284	15.7	587	3	US-08-899-578-2	Sequence 2, Appli
18	275.5	15.2	704	1	US-08-188-582-18	Sequence 18, Appli
19	275.5	15.2	704	1	US-08-646-715-18	Sequence 18, Appli
20	263.5	14.6	439	1	US-08-190-802A-65	Sequence 65, Appli
21	263.5	14.6	798	1	US-08-190-802A-64	Sequence 64, Appli
22	263.5	14.6	798	1	US-08-190-802A-68	Sequence 68, Appli
23	263.5	14.6	798	2	US-08-308-818-2	Sequence 2, Appli
24	263	14.5	318	1	US-08-190-802A-33	Sequence 33, Appli
25	261.5	14.5	514	1	US-08-190-802A-66	Sequence 66, Appli
26	252.5	14.0	713	1	US-08-190-802A-63	Sequence 63, Appli
27	242.5	13.4	343	4	US-09-063-743-5	Sequence 5, Appli

28	240	13.3	305	3	US-08-965-600-1	Sequence 1, Appli
29	240	13.3	375	4	US-09-063-743-1	Sequence 1, Appli
30	235	13.0	409	2	US-08-283-917-3	Sequence 3, Appli
31	235	13.0	409	2	US-08-961-716-3	Sequence 3, Appli
32	235	13.0	410	2	US-08-283-917-9	Sequence 9, Appli
33	235	13.0	410	2	US-08-961-716-9	Sequence 9, Appli
34	225.5	12.5	409	1	US-08-190-802A-51	Sequence 51, Appli
35	217	12.0	517	1	US-08-190-802A-30	Sequence 30, Appli
36	216.5	11.7	906	1	US-08-190-802A-31	Sequence 31, Appli
37	211.5	11.7	2627	2	US-08-751-189-3	Sequence 3, Appli
38	211.5	11.7	2627	2	US-09-060-836-3	Sequence 3, Appli
39	211.5	11.7	2627	4	US-09-184-445-3	Sequence 4, Appli
40	211	11.7	2629	2	US-08-751-189-4	Sequence 4, Appli
41	211	11.7	2629	2	US-09-060-836-4	Sequence 4, Appli
42	211	11.7	2629	4	US-09-184-445-4	Sequence 4, Appli
43	199.5	11.0	376	2	US-08-883-534-5	Sequence 5, Appli
44	199.5	11.0	376	3	US-09-204-764-5	Sequence 5, Appli
45	197.5	10.9	422	1	US-08-190-802A-52	Sequence 52, Appli

ALIGNMENTS

RESULT 1
US-09-180-783-2 Application US/09180783
Sequence 2, Appli 6242181
GENERAL INFORMATION:
APPLICANT: Sifert, Winfried
TITLE OF INVENTION: THE USE OF A GENETIC MODIFICATION IN THE GENE FOR HUMAN
FILE REFERENCE: 1135-2
CURRENT APPLICATION NUMBER: US/09/180,783
CURRENT FILING DATE: 1999-03-17
PCT/EP97/02250
PRIOR FILING DATE: 1997-05-02
PRIOR APPLICATION NUMBER: DE 19619362.1
PRIOR FILING DATE: 1996-05-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-09-180-783-2

Query Match	Best Local Similarity	Score	Pred. No.	DB 4	Length	Indels	Gaps
Matches 328; Conservative	96.5%	1762	5.9e-173	4	340	0	0
QY 1	MGEMEQLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60						
DB 1	MGEMEQLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60						
QY 61	MHWATDSKLLVSASODGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDMM 120						
DB 61	MHWATDSKLLVSASODGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDMM 120						
QY 121	CSYSLKSRGNVKSRELSAHTGYLSGCRFLDNNIVTSSGDTTCALMDIETGOQKTVF 180						
DB 121	CSYSLKSRGNVKSRELSAHTGYLSGCRFLDNNIVTSSGDTTCALMDIETGOQKTVF 180						
QY 181	VGHTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240						
DB 181	VGHTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240						
QY 241	ICTGSDASCRFLDLRADQELTAVSHESIICGITSVAFLSGLRLFAGYDDFNCNVWDSL 300						
DB 241	ICTGSDASCRFLDLRADQELTAVSHESIICGITSVAFLSGLRLFAGYDDFNCNVWDSL 300						
QY 301	KCERVGVLSGHDNRVSCIGVTADGNAVATGSDSFLKIWN 340						
DB 301	KCERVGVLSGHDNRVSCIGVTADGNAVATGSDSFLKIWN 340						

Db 301 KSERVGLSGHNDNRVSCLGVTADGMAVATGSDSFLKIWN 340

RESULT 2

US-08-190-802A-38
Sequence 38, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190, 802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G-Beta 1 bovine, Fig. 21
US-08-190-802A-38

Query Match
Best Local Similarity 87.0%; Score 1573; DB 1; Length 340;
Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

QY 1 MGEMEQKQEAQOLKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
Db 1 MSELQDLQEAQOLKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
QY 61 MHMATDSKLLVASASODGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
Db 61 MHMATDSKLLVASASODGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSYSLKSRGNVAVSRELSTAHGTYLSCCRFLDNNIVTSSGDTTCALMDIETGOQTVF 180
Db 121 CSYSLKSRGNVAVSRELSTAHGTYLSCCRFLDNNIVTSSGDTTCALMDIETGOQTVF 180
QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
Db 181 VGHGTDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
QY 241 ICTGSDASCRFLDLRADQELTAYSHESITIGITSVAFLSGLRLLFAGYDDFNCNWDLSL 300
Db 241 ICTGSDASCRFLDLRADQELTAYSHESITIGITSVAFLSGLRLLFAGYDDFNCNWDLSL 300

QY 301 KCERVGLSGHNDNRVSCLGVTADGMAVATGSDSFLKIWN 340
Db 301 KADRAGVLGAGHNDNRVSCLGVTADGMAVATGSDSFLKIWN 340

RESULT 3

US-08-190-802A-42
Sequence 42, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190, 802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G-Beta 2 (Human), Fig. 25
US-08-190-802A-42

Query Match
Best Local Similarity 84.2%; Score 1523; DB 1; Length 340;
Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGEMEQKQEAQOLKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
Db 1 MSELQDLQEAQOLKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
QY 61 MHMATDSKLLVASASODGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
Db 61 MHMATDSKLLVASASODGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSYSLKSRGNVAVSRELSTAHGTYLSCCRFLDNNIVTSSGDTTCALMDIETGOQTVF 180
Db 121 CSYSLKSRGNVAVSRELSTAHGTYLSCCRFLDNNIVTSSGDTTCALMDIETGOQTVF 180
QY 181 VGHGTDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
Db 181 VGHGTDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
QY 241 ICTGSDASCRFLDLRADQELTAYSHESITIGITSVAFLSGLRLLFAGYDDFNCNWDLSL 300
Db 241 ICTGSDASCRFLDLRADQELTAYSHESITIGITSVAFLSGLRLLFAGYDDFNCNWDLSL 300

Db 241 FTTGSDATCRLFDLRADQELMTSHDNIICGITSVAFSRSGRLLAGYDDFNCNIMDAM 300
QY 301 KCEKRVGLSGHDNRVSLGVTADGMVATGSDSFLKIWN 340
Db 301 KGDAGVLAGHDNRVSLGVTDDGMVATGSDSFLKIWN 340

RESULT 4

US-09-147-826B-2
; Sequence 2, Application US/09147826B
; Patent No. 6251853
; GENERAL INFORMATION:
; APPLICANT: Siffert, Winfried
; TITLE OF INVENTION: PTX-SENSITIVE G PROTEINS, THEIR PREPARATION AND USE
; FILE REFERENCE: 1135-0003
; CURRENT APPLICATION NUMBER: US/09/147, 826B
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: PCT/EP97/04709
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: DE 196 37 518.5
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-147-826B-2

Query Match 84.1%; Score 1520.5; DB 4; Length 299;
Best Local Similarity 85.0%; Pred. No. 3.2e-148;
Matches 289; Conservative 7; Mismatches 3; Indels 41; Gaps 1;

QY 1 MGEMEQKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGHLAKIYA 60
Db 1 MGEMEQKQAEQKQIADARKACADVTLAEVSGLEVGRVQMRTRRLRGHLAKIYA 60
QY 61 MHWATDSKLLVSASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDMM 120
Db 61 MHWATDSKLLVSASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDMM 120
QY 121 CSTYSLKSRGNVKSRELSTAHGTYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 180
Db 121 CSTYSLKSRGNVKSRELSTAHGTYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 180
QY 181 VGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICTFPNGEA 240
Db 181 VGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICTFPNGEA 240
QY 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFSLSGRLLAGYDDFNCNIMDAM 300
Db 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFSLSGRLLAGYDDFNCNIMDAM 300
QY 301 KCEKRVGLSGHDNRVSLGVTADGMVATGSDSFLKIWN 340
Db 301 KCEKRVGLSGHDNRVSLGVTADGMVATGSDSFLKIWN 340

RESULT 5

US-08-190-802A-45
; Sequence 45, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190, 802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33, 875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GTP binding protein (squid), Fig. 28
US-08-190-802A-45

Query Match 81.1%; Score 1467; DB 1; Length 341;
Best Local Similarity 79.9%; Pred. No. 1.2e-142;
Matches 270; Conservative 30; Mismatches 38; Indels 0; Gaps 0;

QY 3 EMEQKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGHLAKIYAMH 62
Db 4 EMEQKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGHLAKIYAMH 62
QY 63 WATDSKLLVSASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDMMCS 122
Db 64 WATDSKLLVSASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDMMCS 122
QY 123 IYSLKSRGNVKSRELSTAHGTYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 182
Db 123 IYSLKSRGNVKSRELSTAHGTYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 182
QY 124 IYSLKTRGNVKSRELSTAHGTYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 183
Db 124 IYSLKTRGNVKSRELSTAHGTYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 183
QY 183 HTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICTFPNGEA 242
Db 183 HTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICTFPNGEA 242
QY 243 TGSDDASCRLFDLRADQELTAYSHESIICGITSVAFSLSGRLLAGYDDFNCNIMDAM 302
Db 243 TGSDDASCRLFDLRADQELTAYSHESIICGITSVAFSLSGRLLAGYDDFNCNIMDAM 302
QY 303 KCEKRVGLSGHDNRVSLGVTADGMVATGSDSFLKIWN 340
Db 303 KCEKRVGLSGHDNRVSLGVTADGMVATGSDSFLKIWN 340

RESULT 6

US-08-190-802A-40
; Sequence 40, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates

STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G- BETA DROSOPH, Fig. 23
US-08-190-802A-40

Query Match 80.3%; Score 1452; DB 1; Length 340;
Best Local Similarity 76.5%; Pred. No. 4.2e-141;
Matches 260; Conservative 38; Mismatches 42; Indels 0; Gaps 0;
QY 1 MGEMEQLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRTLRGLAKIYA 60
DB 1 MNELSLRQEAESLKNARIDARKACADITSLQATSLPIGRIOQMRTRTLRGLAKIYA 60
QY 61 MHWATDSKLVASQDGKLIWDTYTTNKYHAIPLRSSWVMTCAYAPSGNFVACGGLDNM 120
DB 61 MHWGNDSRLVNASQDGKLIWDSHTTNKYHAIPLRSSWVMTCAYAPSGSYVACGGLDNM 120
QY 121 CSIYSLKSRGVNRYKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQOKTVF 180
DB 121 CSIYNLKTREGNVRYSRELPGHGYLSCCRFLDNNIVTSSGDMSCGLMDIETGLQVTSF 180
QY 181 VGHGTDCMSLAVSPDYKFLISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
DB 181 LGHTGDVMAISLAPQCKTFVSGACDASAKLMDIREGVCKQTFPGHESDINAVTFEPNGQA 240
QY 241 ICTGSDASCRLFLRADQELTAYSHESIICGITSVAFSLSGRLLFAGYDDFNCNVWDSL 300
DB 241 FATGSDATCRLFLRADQELTAYSHDNIICGITSVAFSKSGRLLLAGYDDFNCNVWDTM 300
QY 301 KCEKRVGLSGHNRVSCIGVTADGMAVATGSDSFLKIWN 340
DB 301 KAERSGILAGHDNRVSCIGVTENGMAVATGSDSFLRWVN 340

RESULT 7
US-08-190-802A-39
Sequence 39, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G-Beta- bovine (2), Fig. 22
US-08-190-802A-39

Query Match 78.4%; Score 1419; DB 1; Length 326;
Best Local Similarity 78.5%; Pred. No. 9.8e-138;
Matches 260; Conservative 28; Mismatches 33; Indels 10; Gaps 2;
QY 15 KKQIADARKACADITLAEVSGLEVGRVQMRTRTLRGLAKIYAMHWATDSKLVAS 74
DB 1 RNQIADARKACGDSLTITQTAGIDPVGRIOQMRTRTLRGLAKIYAMHWGTSRLVNAS 60
QY 75 QDGKLIWDT-----YTTNKYHAIPLRSSWVMTCAYAPSGNFVACGGLDNMSIYSLKR 129
DB 61 QDGKLIWDSGNVRYTTNKYHAIPLRSSWVMTCAYAPSGNFVACGGLDNISYSLKTR 120
QY 130 EGNVYSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQOKTVFVGHGTDCMS 189
DB 121 -----VSRELPGHTGYLSCCRFLDNNIITSSGDTTCALMDIETGQQTGVPAGHSGDVM 175
QY 190 LAVSPDYKFLISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEAICTGSDAS 249
DB 176 LSLAPDRTFVSGACDASIKLMDVRSRCROTFTGHESDINAVAFPPNGYATFTGSDAT 235
QY 250 CRLFLRADQELTAYSHESIICGITSVAFSLSGRLLFAGYDDFNCNVWDSLKCEKRVGLS 309
DB 236 CRLFLRADQELTAYSHDNIICGITSVAFSRSGRLLLAGYDDFNCNINWDMKGRAGVLA 295
QY 310 GHDRVSCIGVTADGMAVATGSDSFLKIWN 340
DB 296 GHDRVSCIGVTDDGMAVATGSDSFLKIWN 326

RESULT 8
US-09-032-372-1
Sequence 1, Application US/09032372
Patent No. 6008337
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.

```

APPLICANT: Guegler, Karl J.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,372
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-0478 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 78191
US-09-032-372-1

```

```

Query Match 52.3%; Score 946.5; DB 3; Length 395;
Best Local Similarity 51.9%; Pred. No. 4.7e-89;
Matches 177; Conservative 56; Mismatches 103; Indels 5; Gaps 3;

QY 4 MEQLKQAEOLKQIADARKACADITLAEIVSGLEVGRVQMRTRRLRGLAKIYAMHW 63
DB 54 LASLKEASESLKGLKEERAKLHDELHQAERVEALGQFVMTKRTLKGHGKVKLCMDW 113
QY 64 ATDSKLVASASQDGLIWDYTTNKVHAIFLRSSWMTCAVAPSGNFVACGGGLDMCST 123
DB 114 CKDKRRIVSSQDGKVIWDSFTTNKEHAVTMCWTMACAYAPSGCAIACGGGLDNKCSV 173
QY 124 YSL--KSREGNAVYSRELSAHTGYLSCRFID--DNNIVTSSGDTTCALMDIETGQOKTVF 180
DB 174 YPLTFDKNENMAARKKSVAMHTNYLSACSFNSDMQILITASGDGTALMDVESGQLLOSF 233
QY 181 VGHGTGD--CMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAI CFFPNG 238
DB 234 HGHGADVLCLDLAPSETGNTFVSGGCDKAMWDMRSGQCVQAFETHESDINSVRYPSG 293
QY 239 EAICTGSDDASCRLFDLRADQELTAYSHESITIGITSVAFLSGRLTFAGYDDFNENWMD 298
DB 294 DAFASGSDATCRLYDLRADREVAIYSKESITFGASSVDLSLGRLLFAGYNDYINWMD 353
QY 299 SLKCEKRVGLSGHNRVSCLGVTADGMAVATGSDWSFLKIM 339
DB 354 VLKGRVSVILFGHENRVSTLRVSPDGTAFCSGSDHDLRLRW 394

```

```

RESULT 9
US-08-190-802A-61
Sequence 61, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: STE4 - YEAST, Fig. 44
US-08-190-802A-61

```

```

Query Match 35.3%; Score 639; DB 1; Length 423;
Best Local Similarity 36.3%; Pred. No. 2.1e-57;
Matches 139; Conservative 74; Mismatches 124; Indels 46; Gaps 6;

QY 3 EMEQLKQAEOLKQIADARKACADITLAEIVSGLEV--GRVQMRTRRLRGLAKIYA 60
DB 38 KIEARQESKQLHAQINKAKKHQDASLFQMANKYVSLTKNKINLKPNIVLKGNKISD 97
QY 61 MHMATDSKLLVASASQDGLIWDYTTNKVHAIFLRSSWMTCAVAPSGNFVACGGGLDM 120
DB 98 FRWSRDSKRILSASQDGFMLIWDASGLKQNAIPLDGQVLSALSPSSFLVASAGLNN 157
QY 121 CSIYSLKREGNV--KVSRELSAHTGYLSCRFID--DNNIVTSSGDTTCALMDIETGQOKT 178
DB 158 CTIYRV--SKENRVAQNVASIFRGHTCYISDIEFTDNLHLLTASGDMTCALMDIPKAKRVR 216
QY 179 VEVGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAI 232
DB 217 EYSDHLGDVLAALPEEPNLENSNTFASCGSDGYTYIWDSPSPAVQSFYVNDSDINAL 276
QY 233 CFFPNGEAICTGSDDASCRLFDLRADQEL-----TAYSH 266
DB 277 RFFKDGMSIYVAGSDNGAINMYDLSDCSITATPSLFRGYERTPTTYMAANMEYNTAOSP 336
QY 267 ESIIC-----GITSVAFLSGRLTFAGYDDFNENWMDSLKCEKRVGLSGHNRVSC 317
DB 337 QTLKSTSSSYLDNGGVSLDFSGAGRLMYSCTYDIGCVWVYVLEKGEIVGKLEGGHGRVTG 396

```



```

RESULT 13
US-08-190-802A-62
; Sequence 62, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: TRANSCRIPTION FACTOR TTF, Fig. 45
US-08-190-802A-62

```

Query Match	16.3%;	Score 295;	DB 1;	Length 704;	
Best Local Similarity	27.8%;	Pred. No. 9.8e-22;			
Matches	88;	Conservative 51;	Mismatches 133;	Indels 44;	Gaps 9;
QY	55	LAKIYAMHWATDSKLLVSA	SGDKLIWDTYTTNKVHA	IPLRSSWMTCA-YAPSGN	EVA 113
		: : : : :	:	: :	
Db	345	LKKKALREAS-KRLALSKD	QLPSAVE---YTV-----	LNSHGGVTCALSIDSD	TMLA 393
QY	114	CGGLDNMCSTYSL-----	KSREGNVK-----	VSRELSAHTGYL	146
		: : : :	: : :	: :	
Db	394	CGFGDSSVRIWSLTPAN	VRIPLKDADSLRELDKES	ADINVRMLDDRSGEVTR	SLMGHTGPV 453
QY	147	SCREFLDNNIVTS-SGDT	FCALWDIETGOQKTVFV	GHTGDCMSLAVSPDYK	LFIGACD 205
		: : : : :	: : :	: : : : :	
Db	454	YRCFAFAPENMLLLSC	SEDSITRLMSLLTWSC	VVTVYRGHVPYWDYR	FAFPHGYFVSCSYD 513
QY	206	ASAKLMDVREGTCRQT	FTGHESDINAI	CFEPNGEAICTGSDAS	CRFLDLRADQELTAYS 265
		: : : :	: : :	: : :	
Db	514	KTARLWATDSNOALR	VEVGHLSVDYCVQFH	PNSNYVATGSSDRTV	RLWDMNMTGQSVRLMT 573
QY	266	-HESIIGITVAFSLSG	RLLFAGYDDFNCNVW	DSLKCERYGLSGHDNR	VSCLGVTADG 324
		: : :	: :	: : : :	
Db	574	GHKG---SVSSLA	FSACGRYLASGSVD	HNIIWDL	SGSLVTTLLRHTSTVTTITFSRDG 630
QY	325	MAVATGSWDSFLKIWN	340		
		: : : :			
Db	631	TVLAAAGLDNNLT	LMD 646		

Db 454 YRCAFAPEMNLISCSEDSTIRLWSILLTWSVCVTRYGHVYPWMDVRFAPHGYFVSCSYD 513
QY 206 ASAKLMDVREGTCROTFTGHESDINAICEFPNGEAICTGSDDASCRLEFDLRADQELTAYS 265
Db 514 KTARLWATDSNOALRVEVGHLSVDVDCVQFHPNSNYVATGSSDRTVRLWDMNMTGQSVRLMT 573
QY 266 -HESIICGITSVAFSLSGRLLFAGYDDFN CNWWSLKCERYGVLSGHDNRVSCLGVTADG 324
Db 574 GHKG---SVSSLAFSACGRYLAAGSVVDHNIILWDLNSGSLVTTLLRHTSTVTITTFESRDG 630
QY 325 MAVATGSWDSFLKIWN 340
Db 631 TVLAAAGLDNNTLWMD 646

Search completed: September 28, 2001, 10:28:39
Job time: 30 sec

Fri Sep 28 10:45:09 2001

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:29:45 ; Search time 16.71 Seconds
(without alignments)
697.000 Million cell updates/sec

Title: US-09-492-029-3
Perfect score: 1809
Sequence: 1 MGMEQLKQAEQLKKQLAD.....TADGMAVATGSMDSFLKIMN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1809	100.0	340	1	GBB3_RAT
2	1794	99.2	340	1	GBB3_MOUSE
3	1771	97.9	340	1	GBB3_CANFA
4	1762	97.4	340	1	GBB3_HUMAN
5	1573	87.0	340	1	GBB1_XENLA
6	1568	86.7	340	1	GBB1_RAT
7	1566	86.6	340	1	GBB2_HUMAN
8	1523	84.2	340	1	GBB2_MOUSE
9	1516	83.8	340	1	GBB1_HUMAN
10	1515	83.7	340	1	GBB1_MOUSE
11	1495	82.6	340	1	GBB4_MOUSE
12	1493	82.5	341	1	GBB1_MOUSE
13	1482	81.9	340	1	GBB1_HUMAN
14	1477	81.6	340	1	GBB2_BOVIN
15	1467	81.1	341	1	GBB1_MOUSE
16	1467	81.1	341	1	GBB1_MOUSE
17	1452	80.3	340	1	GBB1_MOUSE
18	1452	80.3	340	1	GBB1_MOUSE
19	1225	67.7	347	1	GBB1_MOUSE
20	1189	65.7	359	1	GBB1_MOUSE
21	946.5	52.3	353	1	GBB5_MOUSE
22	945.5	52.3	353	1	GBB5_MOUSE
23	939.5	51.9	356	1	GBB5_MOUSE
24	844	46.7	380	1	GBB5_MOUSE
25	828	45.8	380	1	GBB5_MOUSE
26	826	45.7	377	1	GBB5_MOUSE
27	826	45.7	377	1	GBB5_MOUSE
28	825	45.6	377	1	GBB5_MOUSE
29	817	45.2	346	1	GBB2_MOUSE
30	817	45.2	346	1	GBB2_MOUSE
31	792	43.8	377	1	GBB2_MOUSE
32	663	36.7	305	1	GBB2_MOUSE
33	635	35.1	423	1	GBB2_MOUSE

RESULT	1	STANDARD	PRT	340 AA.
GBB3_RAT	383.5	21.2	1356	1
GBB3_RAT	341.5	18.9	742	1
GBB3_RAT	305.5	16.9	465	1
GBB3_RAT	304.5	16.8	361	1
GBB3_RAT	302	16.7	316	1
GBB3_RAT	300.5	16.6	317	1
GBB3_RAT	297.5	16.4	317	1
GBB3_RAT	295.5	16.3	317	1
GBB3_RAT	295	16.3	362	1
GBB3_RAT	294	16.3	704	1
GBB3_RAT	293.5	16.2	554	1
GBB3_RAT			318	1

ALIGNMENTS

GBB3_RAT	P52287	01-OCT-1996 (Rel. 34, Created)	HEP1_PODAN	Q00808	podospira a
GBB3_RAT	P52287	01-OCT-1996 (Rel. 34, Last sequence update)	PKWA_THECU	P49695	thermomomys
GBB3_RAT	P52287	01-OCT-1996 (Rel. 34, Last annotation update)	PRO4_YEAST	P20053	saccharomyc
GBB3_RAT	P52287	15-JUL-1998 (Rel. 36, Last annotation update)	WDS_DROME	Q9V3J8	drosophila
GBB3_RAT	P52287	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3	GBLP_BIOGL	Q93134	biomphalari
GBB3_RAT	P52287	(TRANSDUCIN BETA CHAIN 3)	GBLP_BRARE	Q42248	brachydanio
GBB3_RAT	P52287	GNB3	GBLP_HUMAN	P25388	homo sapien
GBB3_RAT	P52287	Rattus norvegicus (Rat)	GBLP_ORENI	Q42249	oreochromis
GBB3_RAT	P52287	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	WDR5_HUMAN	Q9UGP9	homo sapien
GBB3_RAT	P52287	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	T2D4_DROME	P49846	drosophila
GBB3_RAT	P52287	NCBI_TaxID=10116;	PRO4_ARATH	Q22212	arabidopsis
GBB3_RAT	P52287	SEQUENCE FROM N.A.	GBLP_TRYBB	Q94775	trypanosoma
GBB3_RAT	P52287	STRAIN=SPRAGUE-DAWLEY; TISSUE=Heart;			
GBB3_RAT	P52287	MEDLINE=95047499; PubMed=7959013;			
GBB3_RAT	P52287	Ray K., Robishaw J.D.;			
GBB3_RAT	P52287	"Cloning and sequencing of a rat heart cDNA encoding a G-protein beta			
GBB3_RAT	P52287	subunit related to the human retinal beta 3 subunit."			
GBB3_RAT	P52287	Gene 149:337-340(1994).			
GBB3_RAT	P52287	-1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE			
GBB3_RAT	P52287	INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE			
GBB3_RAT	P52287	SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR PROTEIN-			
GBB3_RAT	P52287	ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-			
GBB3_RAT	P52287	RECEPTOR INTERACTION.			
GBB3_RAT	P52287	-1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).			
GBB3_RAT	P52287	-1- TISSUE SPECIFICITY: EXPRESSED AT A HIGH LEVEL IN THE HEART AND AT			
GBB3_RAT	P52287	A MUCH LOWER LEVEL IN THE BRAIN.			
GBB3_RAT	P52287	-1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).			
GBB3_RAT	P52287	This SWISS-PROT entry is copyright. It is produced through a collaboration			
GBB3_RAT	P52287	between the Swiss Institute of Bioinformatics and the EMBL outstation			
GBB3_RAT	P52287	the European Bioinformatics Institute. There are no restrictions on its			
GBB3_RAT	P52287	use by non-profit institutions as long as its content is in no way			
GBB3_RAT	P52287	modified and this statement is not removed. Usage by and for commercial			
GBB3_RAT	P52287	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
GBB3_RAT	P52287	or send an email to license@isb-sib.ch).			
GBB3_RAT	P52287	EMBL: L29090; AAA62620.1; --			
GBB3_RAT	P52287	HSSP: P04901; 1TBG.			
GBB3_RAT	P52287	InterPro: IPR001632; --			
GBB3_RAT	P52287	InterPro: IPR001680; --			
GBB3_RAT	P52287	Pfam: PF00400; WD40; 7.			
GBB3_RAT	P52287	PRINTS: PR00319; GPROTEINB.			
GBB3_RAT	P52287	PRINTS: PR00320; GPROTEINB.			
GBB3_RAT	P52287	PROSITE: PS00678; WD_REPEATS_1; 3.			
GBB3_RAT	P52287	PROSITE: PS50082; WD_REPEATS_2; 5.			
GBB3_RAT	P52287	PROSITE: PS50294; WD_REPEATS_REGION; 1.			
GBB3_RAT	P52287	Transducer; Repeat; WD repeat; Multigene family.			
GBB3_RAT	P52287	REPEAT	53	83	WD 1.
GBB3_RAT	P52287	REPEAT	95	125	WD 2.
GBB3_RAT	P52287	REPEAT	141	170	WD 3.
GBB3_RAT	P52287	REPEAT	182	212	WD 4.
GBB3_RAT	P52287	REPEAT	224	254	WD 5.

FT REPEAT 268 298 WD 6.
 REPEAT 310 340 WD 7.
 SO SEQUENCE 340 AA; 37180 MW; 020A41F754E4B1DA CRC64;

Query Match
 Best Local Similarity 100.0%; Score 1809; DB 1; Length 340;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMEQLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRLRGLAKIYA 60
 DB 1 MGEMEQLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRLRGLAKIYA 60
 QY 61 MHMATDSKLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 DB 61 MHMATDSKLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 QY 121 CSIYSLKSRGNVKSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQOKTVE 180
 DB 121 CSIYSLKSRGNVKSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQOKTVE 180
 QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
 DB 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELTAHSHESIIGITSVAFLSGRLTFAGYDDFNCNVWDSL 300
 DB 241 ICTGSDASCRLFDLRADQELTAHSHESIIGITSVAFLSGRLTFAGYDDFNCNVWDSL 300
 QY 301 KCERVGLSGHNRVSCIGVTADGMAVATGSWDSFLKIWN 340
 DB 301 KCERVGLSGHNRVSCIGVTADGMAVATGSWDSFLKIWN 340

RESULT 2
 GBB3_MOUSE

ID GBB3_MOUSE STANDARD; PRT; 340 AA.
 AC 061011;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 3
 GN GNB3.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
 RA Lu J., Gorrell J.H., Chinnault A.C., Belmont J.W., Miller W.,
 RA Gibbs R.A.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE OF 199-301 FROM N.A.
 RC STRAIN=CF-1 / HARLAN; TISSUE=Retina;
 RX MEDLINE=97011591; PubMed=8858601;
 RA Williams C.J., Schultz R.M., Kopf G.S.;
 RT "G protein gene expression during mouse oocyte growth and maturation,
 RT and preimplantation embryo development.";
 RL Mol. Reprod. Dev. 44:315-323(1996).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: AC002397; AAC36013.1; ..
 DR EMBL: U38494; AAB01725.1; ..
 DR HSSP: P04901; 1GP2.
 DR MGI: 95785; Gnb3.
 DR InterPro: IPR001632; ..
 DR InterPro: IPR001680; ..
 DR Pfam: PF00400; WD40; 2.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINB.
 DR PROSITE: PS00678; WD_REPEATS_1; 3.
 DR PROSITE: PS50082; WD_REPEATS_2; 5.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SO SEQUENCE 340 AA; 37240 MW; 44BA0F8C0FEDEEB1 CRC64;

Query Match
 Best Local Similarity 99.2%; Score 1794; DB 1; Length 340;
 Matches 336; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGEMEQLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRLRGLAKIYA 60
 DB 1 MGEMEQLKQAEQKQIADARKACADITLAEVSGLEVGRVQMRTRLRGLAKIYA 60
 QY 61 MHMATDSKLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 DB 61 MHMATDSKLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 QY 121 CSIYSLKSRGNVKSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQOKTVE 180
 DB 121 CSIYSLKSRGNVKSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQOKTVE 180
 QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
 DB 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELTAHSHESIIGITSVAFLSGRLTFAGYDDFNCNVWDSL 300
 DB 241 ICTGSDASCRLFDLRADQELTAHSHESIIGITSVAFLSGRLTFAGYDDFNCNVWDSL 300
 QY 301 KCERVGLSGHNRVSCIGVTADGMAVATGSWDSFLKIWN 340
 DB 301 KCERVGLSGHNRVSCIGVTADGMAVATGSWDSFLKIWN 340

RESULT 3
 GBB3_CANFA

ID GBB3_CANFA STANDARD; PRT; 340 AA.
 AC P79147;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 3
 GN GNB3.

OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-ALASKAN MALAMUTE; TISSUE=Retina;
 RX MEDLINE=97409956; PubMed=9266671;
 RA Akhmedov N.B., Piriev N.I., Ray K., Acland G.M., Aguirre G.D.,
 RA Farber D.B.;
 RT "Structure and analysis of the transducin beta3-subunit gene, a
 RT candidate for inherited cone degeneration (cd) in the dog.";
 RL Gene 194:47-56(1997).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U52916; AAC48760.1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 5.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37144 MW; 8E3B5A5238E29C37 CRC64;

Query Match 97.98; Score 1771; DB 1; Length 340;
 Best Local Similarity 97.4%; Pred. No. 5.1e-148;
 Matches 331; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGEMEQLRQAEQKQIADARACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
 DB 1 MGEMEQLRQAEQKQIADARACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
 QY 61 MHWATDSKLLVSASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSSGNEVACGLDMM 120
 DB 61 MHWATDSKLLVSASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSSGNEVACGLDMM 120
 QY 121 CSITSLKREGNKKVRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 180
 DB 121 CSITSLKREGNKKVRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 180
 QY 181 VGHTEGDCMSLAVSPDYKLEISGACDASAKLWDVREGTCROTFTGHESDINAICTFPNGEA 240
 DB 181 VGHTEGDCMSLAVSPDYKLEISGACDASAKLWDVREGTCROTFTGHESDINAICTFPNGEA 240
 QY 241 ICTGSDDASCRLFLRADQELTAISHESIICGTSVAFLSGRLFFAGYDDFNCNWNWDSL 300
 DB 241 ICTGSDDASCRLFLRADQELTAISHESIICGTSVAFLSGRLFFAGYDDFNCNWNWDSL 300
 QY 301 KGERVGVLSGHDNRVSCIGVTADGMAVATGSDSFLKIWN 340
 DB 301 KGERVGVLSGHDNRVSCIGVTADGMAVATGSDSFLKIWN 340

RESULT 4
 GBB3_HUMAN
 ID GBB3_HUMAN STANDARD; PRT; 340 AA.
 AC P16520;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 3
 DE (TRANSDUCIN BETA CHAIN 3).
 GN GNB3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90192801; PubMed=2107550;
 RA Levine M.A., Smallwood P.M., Moen P.T. Jr., Helman L.J., Ahn T.G.;
 RT "Molecular cloning of beta 3 subunit, a third form of the G protein
 RT beta-subunit polypeptide."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2329-2333(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96303695; PubMed=8723724;
 RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E.,
 RA Spanos S., Malley T., Gibbs R.A.;
 RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
 RT genes at human chromosome 12p13."
 RL Genome Res. 6:314-326(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Busch S., Dyhr W., Siffert W.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M31328; AAA52582.1; -.
 DR EMBL; U47924; AAB51313.1; -.
 DR EMBL; Y12050; CAA72779.1; -.
 DR EMBL; Y12051; CAA72779.1; JOINED.
 DR EMBL; Y12052; CAA72779.1; JOINED.
 DR EMBL; Y12053; CAA72779.1; JOINED.
 DR EMBL; Y12054; CAA72779.1; JOINED.
 DR EMBL; Y12055; CAA72779.1; JOINED.
 DR EMBL; Y12056; CAA72779.1; JOINED.
 DR EMBL; Y12057; CAA72779.1; JOINED.
 DR EMBL; Y12058; CAA72779.1; JOINED.
 DR EMBL; U47930; AAC50468.1; -.
 DR PIR; A35096; RGHUB3.
 DR HSSP; P04901; ITBG.
 DR MIM; 139130; -.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 5.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.

FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37221 MW; 896E706A61B8D74F CRC64;

Query Match 97.4%; Score 1762; DB 1; Length 340;
 Best Local Similarity 96.5%; Pred. No. 3.1e-147;
 Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEQLKQAEQLKKQIADARKACADITLAEVSGLEVGVQMRTRLRGLAKIYA 60
 DB 1 MGEMEQLKQAEQLKKQIADARKACADVTLAELVSGLEVGVQMRTRLRGLAKIYA 60
 QY 61 MHMATDSKLVASASQDGKLIWDPYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 DB 61 MHMATDSKLVASASQDGKLIWDSYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 QY 121 CSIYSLKREGNVKVSRELSAHTGYSCLCCFLDDNNITVSSGDTTCALMDIETGQKTVF 180
 DB 121 CSIYNLKSREGNVKVSRELSAHTGYSCLCCFLDDNNITVSSGDTTCALMDIETGQKTVF 180
 QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQTFGHSIDINAIICFPNGEA 240
 DB 181 VGHGDCMSLAVSPDENLFISSGACDASAKLMDVREGTCRQTFGHSIDINAIICFPNGEA 240
 QY 241 ICTGSDASCRLFLRADQELTAYSHESIICGITSVAFSLSGRLIFAGYDDFNCNVWDSL 300
 DB 241 ICTGSDASCRLFLRADQELTAYSHESIICGITSVAFSLSGRLIFAGYDDFNCNVWDSL 300
 QY 301 KCERVGVLGHDNRVSCGLVTADGMAVATGWSWDSFLKIWN 340
 DB 301 KSERVGILSGHDNRVSCGLVTADGMAVATGWSWDSFLKIWN 340

RESULT 5
 GBB1_HUMAN STANDARD; PRT; 340 AA.
 AC P04901; P04697;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1
 DE (TRANSDUCIN BETA CHAIN 1).
 GN GNB1.
 OS Homo sapiens (Human), Mus musculus (Mouse), Bos taurus (Bovine), and
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606, 10090, 9913, 9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Liver;
 RX MEDLINE=87030912; PubMed=3095147;
 RA Codina J., Stengel D., Woo S.L.C., Birnbaumer L.;
 RT "Beta-subunits of the human liver Gs/Gi signal-transducing proteins
 RT and those of bovine retinal rod cell transducin are identical.";
 RL FEBS Lett. 207:187-192(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Mouse; TISSUE=Adrenal gland;
 RA Qiu R., Schimmer B.P.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Bovine;
 RX MEDLINE=86177563; PubMed=3083416;
 RA Fong H.K.W., Hurley J.B., Hopkins R.S., Maize-Lye R., Johnson M.S.,
 RA Doolittle R.F., Simon M.I.;

RT "repetitive segmental structure of the transducin beta subunit:
 RT homology with the CDC4 gene and identification of related mRNAs";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:2162-2166(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Bovine;
 RX MEDLINE=86030675; PubMed=2414128;
 RA Sugimoto K., Nukada T., Tanabe T., Takahashi H., Noda M., Minamino N.,
 RA Kangawa K., Matsuo H., Hirose T., Inayama S., Numa S.;
 RT "Primary structure of the beta-subunit of bovine transducin deduced
 RT from the cDNA sequence";
 RL FEBS Lett. 191:235-240(1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.familiaris;
 RX MEDLINE=97445667; PubMed=9300552;
 RA Kyliana T., Paulin L., Hurwitz M.Y., Hurwitz R.L., Komonen B.;
 RT "Cloning of the cDNA encoding rod photoreceptor
 RT cGMP-phosphodiesterase alpha and gamma subunits from the retinal
 RT degenerate Labrador retriever dog";
 RL Res. Vet. Sci. 62:293-296(1997).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF HETEROTRIMER.
 RX MEDLINE=96107343; PubMed=8521505;
 RA Wall M.A., Coleman D.E., Lee E., Iniguez-Lluhi J.A., Posner B.A.,
 RA Gilman A.G., Sprang S.R.;
 RT "The structure of the G protein heterotrimer Gi alpha 1 beta 1 gamma
 RT 2.";
 RL Cell 83:1047-1058(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF BETA-GAMMA DIMER.
 RX MEDLINE=96149254; PubMed=8552196;
 RA Sondek J., Bohm A., Lambright D.G., Hamm H.E., Sigler P.B.;
 RT "Crystal structure of a G-protein beta gamma dimer at 2.1-A
 RT resolution";
 RL Nature 379:369-374(1996).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH PHOSDUCIN.
 RX MEDLINE=98416696; PubMed=9739091;
 RA Loew A., Ho Y.K., Blundell T., Bax B.;
 RT "Phosducin induces a structural change in transducin beta gamma";
 RL Structure 6:1007-1019(1998).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X04526; CAA28207.1; -
 DR EMBL; U29055; AAC52905.1; -
 DR EMBL; X03073; CAA26875.1; -
 DR EMBL; M13236; AAA30792.1; -
 DR EMBL; M36430; AAA63265.1; -
 DR EMBL; Z75134; CAA99446.1; -
 DR PIR; A24853; RGHUB1.
 DR PIR; A24225; RGHOB1.
 DR PDB; 1GG2; 12-FEB-97.
 DR PDB; 1GP2; 12-FEB-97.
 DR PDB; 1TBG; 01-APR-97.
 DR PDB; 1A0R; 16-FEB-99.
 DR PDB; 1B9X; 23-FEB-99.
 DR PDB; 1B9Y; 23-FEB-99.
 DR MIM; 139380; -

DR MGD; MGI:95781; Gnb1.
 DR InterPro; IPR001632; -
 DR InterPro; IPR001680; -
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PRO0319; GPROTEINB.
 DR PRINTS; PRO0320; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS00682; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 DR Transducer; Repeat; WD repeat; Multigene family; 3D-structure.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT CONFLICT 71 71 V -> L (IN REF. 4).
 SQ SEQUENCE 340 AA; 37377 MW; 896CB32D2686598 CRC64;

Query Match 87.0%; Score 1573; DB 1; Length 340;
 Best Local Similarity 83.2%; Pred. No. 1.2e-130;
 Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

QY 1 MGEMEQLEAEQLEKQIADARKACADITLAEVSGLEVGVQVQMTTRTLRGHLAKIYA 60
 DB 1 MSELQDLROEAEQLEKQIADARKACADATLSQITNNIDVGRIGQMTTRTLRGHLAKIYA 60
 QY 61 MHWTDSKLVSASODGKLIVMDYTTNNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
 DB 61 MHWTDSKLVSASODGKLIVMDYTTNNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
 QY 121 CSIYSLKREGNVKVSRELSTHTGYLSCCRFLDNNITVSSGDTTCALWDIETGQQTTF 180
 DB 121 CSIYSLKREGNVKVSRELSTHTGYLSCCRFLDNNITVSSGDTTCALWDIETGQQTTF 180
 QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICTFPNGEA 240
 DB 181 TGHGDMVSLAPDTRLEFVSGACDASAKLMDVREGTCRQFTGHESDINAICTFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESIIGITSVAFSLGRLPAGYDDFNCNVWDSL 300
 DB 241 FATGSDATCRLFDLRADQELMTYSHDNITIGITSVSFSKSGRLLAGYDDFNCNVWDSL 300
 QY 301 KCERYGVLSGHDNRVSCGLVTADGMAVATGSWDSFLKIWN 340
 DB 301 KADRAGVLAGHDNRVSCGLVTDDGMAVATGSWDSFLKIWN 340

RESULT 6
 GBL_XENLA
 ID GBL_XENLA STANDARD; PRT; 340 AA.
 AC P79959;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1
 DE (TRANSDUCIN BETA CHAIN 1) (XGBETA1).
 GN GNB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97109512; PubMed=8951792;
 RA Devic E., Paqueret L., Rizzotti K., Monier A., Knibiehler B.,
 RA Audigier Y.;
 RT "The mRNA encoding a beta subunit of heterotrimeric GTP-binding
 RT proteins is localized to the animal pole of Xenopus laevis oocyte and
 RT embryos.";

RL Mech. Dev. 59:141-151(1996).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X86969; CAA60532.1; -
 DR HSSP; P04901; 1TBG.
 DR InterPro; IPR001632; -
 DR InterPro; IPR001680; -
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PRO0319; GPROTEINB.
 DR PRINTS; PRO0320; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS00682; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37330 MW; DE036FEF60A2D6A9 CRC64;

Query Match 86.7%; Score 1568; DB 1; Length 340;
 Best Local Similarity 82.9%; Pred. No. 3.2e-130;
 Matches 282; Conservative 30; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGEMEQLEAEQLEKQIADARKACADITLAEVSGLEVGVQVQMTTRTLRGHLAKIYA 60
 DB 1 MSELQDLROEAEQLEKQIADARKACADATLSQITANNIDVGRIGQMTTRTLRGHLAKIYA 60
 QY 61 MHWTDSKLVSASODGKLIVMDYTTNNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
 DB 61 MHWTDSKLVSASODGKLIVMDYTTNNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
 QY 121 CSIYSLKREGNVKVSRELSTHTGYLSCCRFLDNNITVSSGDTTCALWDIETGQQTTF 180
 DB 121 CSIYSLKREGNVKVSRELSTHTGYLSCCRFLDNNITVSSGDTTCALWDIETGQQTTF 180
 QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICTFPNGEA 240
 DB 181 TGHGDMVSLAPDTRLEFVSGACDASAKLMDVREGTCRQFTGHESDINAICTFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESIIGITSVAFSLGRLPAGYDDFNCNVWDSL 300
 DB 241 FATGSDATCRLFDLRADQELMTYSHDNITIGITSVAFSLGRLLAGYDDFNCNVWDSL 300
 QY 301 KCERYGVLSGHDNRVSCGLVTADGMAVATGSWDSFLKIWN 340
 DB 301 KADRAGVLAGHDNRVSCGLVTDDGMAVATGSWDSFLKIWN 340

RESULT 7
 GBL_RAT
 ID GBL_RAT STANDARD; PRT; 340 AA.
 AC P54311;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

	Transducer;	Repeat;	WD repeat;	Multigene family.
KW	REPEAT	53	83	WD 1.
FT	REPEAT	95	125	WD 2.
FT	REPEAT	141	170	WD 3.
FT	REPEAT	182	212	WD 4.
FT	REPEAT	224	254	WD 5.
FT	REPEAT	268	298	WD 6.
FT	REPEAT	310	340	WD 7.
FT	CONFLICT	195	195	D -> N (IN REF. 2).
FT	SEQUENCE	340 AA;	37331 MW;	5D08FFA240ADDEE6 CRC64,

Query Match	84.28;	Score 1523;	DB 1;	Length 340;
Best Local Similarity	80.98;	Pred. No. 2.8e-126;		
Matches 275; Conservative	31;	Mismatches 34;	Indels 0;	Gaps 0;

[illegible]

RESULT	9
ID	GBB2_MOUSE
STANDARD;	PRT;
340 AA.	
AC	P54312;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, last sequence update)
DT	01-OCT-2000 (Rel. 40, last annotation update)
DE	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 2
DE	(TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT).
GN	GNB2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/KAPLAN;
RA	Kuroda S., Tokunaga C., Konishi H., Kikkawa U.;
RL	Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE OF 182-297 FROM N.A.
RC	STRAIN=CF1;
RX	MEDLINE=97011591; PubMed=8858601;
RA	Williams C.J., Schultz R.M., Kopf G.S.;
RT	"G protein gene expression during mouse oocyte growth and maturation,
RT	and preimplantation embryo development.";
RT	Mol. Reprod. Dev. 44:315-323(1996).
CC	-I- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC	INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC	SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC	GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN
CC	EFFECTOR INTERACTION.

--
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN MEIOTICALLY INCOMPETENT OOCYTES.
CC
CC EXPRESSION INCREASES IN FULLY GROWN MEIOTICALLY COMPETENT OOCYTES.
CC
CC EXPRESSION THEN DECREASES DURING METAPHASE-II ARRESTED EGGS, ONE-
CC CELL EMBRYO, TWO-CELL EMBRYO AND EIGHT-CELL EMBRYO STAGES, AND
CC INCREASES AGAIN DURING BLASTOCYST STAGE.
CC
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outpost on its
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

CC	EMBL; U34960; AAC72250.1; -
DR	EMBL; U38505; AAB01736.1; -
DR	HSSP; P04901; ITBG.
DR	MGI; MGI:95784; Gnb2.
DR	InterPro; IPR001632; -
DR	InterPro; IPR001680; -
DR	Pfam; PF00400; WD40; 7.
DR	PRINTS; PR00319; GPOTEINB.
DR	PRINTS; PR00320; GPOTEINBRPT.
DR	PROSITE; PS00678; WD_REPEATS_1; 3.
DR	PROSITE; PS00682; WD_REPEATS_2; 6.
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW	Transducer; Repeat; WD repeat; Multigene family; Polymorphism
FT	REPEAT 53 83 WD 1.
FT	REPEAT 95 125 WD 2.
FT	REPEAT 141 170 WD 3.
FT	REPEAT 182 212 WD 4.
FT	REPEAT 224 254 WD 5.
FT	REPEAT 268 298 WD 6.
FT	REPEAT 310 340 WD 7.
FT	VARIANT 248 248 S -> A (IN STRAIN CF1).
SEQ	SEQUENCE 340 AA: 37333 MW: FEC7DB4F9BA3737D CRC64;

Query Match	83.88;	Score 1516;	DB 1;	Length 340;
Best Local Similarity	80.38;	Pred. No. 1.2e-125;		
Matches 273;	Conservative	32;	Mismatches 35;	Indels 0;
				Gaps 0;
QY	1 MGEMEQLKQEAQLKKQIADARRKACADITLAEVLVSGLEVGVRVQMRTRRTLGLHLAKIYA	60		
Db	1 MSELQQLQEAQLRNQIRDARRKAGDSTLTQITAGLDPEVGRIQMRTRTLGLHLAKIYA	60		
QY	61 MHMATDSKLLVASAQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM	120		
Db	61 MHWGTDSRLLYVASAQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNT	120		
QY	121 CSIYSLKSRREGNAVYSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQOKTVE	180		
Db	121 CSIYSLKTRREGNAVYSRELPGHTGYLSCCRFLDDNQITSSGDTTCALMDIETGQQTVE	180		
QY	181 VGHGTGDCMSLAVSPDYKLLFISGACDASAKIMDVREGTCROTFTGHESDINAICFFPNGEA	240		
Db	181 AGHSGDVMSLSLAPDGRFTVSGACDASIKIMDVRODSMCROTFTGHESDINAAVFFPNGYA	240		
QY	241 ICTGSDDASCRLFDLRADQDELTAYSHESIICGITSVAFSLSGRLLFAGYDDENCNVWDSL	300		
Db	241 FTTGSDDSTCRLFDLRADQDELIMYSHDNIIICGITSVAFSRSGRLLLAGYDDENCNIWDAM	300		
QY	301 KCERVAVGLSGHDNRVSCLGVTADGMAVATGSWDSFLKIWN	340		
Db	301 KGDRAGVLAGHDNRVSCLGVTDDCGMAVATGSWDSFLKIWN	340		

```

RESULT 10
GBB1_CAEEL
ID GBB1_CAEEL STANDARD;
AC P17343; Q19394;
PRT; 340 AA

```

```

Db      61  MHMASDSRNLVSASQDGKLIWDSYTTNKVHAIPLRSSWMVTCAYAPSGSFVACGGLDNI 120
QY      121  CSTYSLKSRREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 180
Db      121  CSTYSLKTRREGNVKVSRELPGHGTGYLSCCRFLDDNQIVTSSGDMTCALWDIETGQOCTAF 180
QY      181  VGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESHEDINAICFPNGEA 240
Db      181  TGHGTGDMVSLSTSPDFRTFISGACDASAKLMDIRDGMCKQTFPGHESDINAVAFPPSGNR 240
QY      241  ICTGSDDASCREFDLRADQELTAYSHESIIGITSVAFSLSGRLTFAGYDDFNCNVWDSL 300
Db      241  FATGSDDATCRFLDIRADQELAMYSHDNIICGITSVAFSKSGRLTFAGYDDFNCNVWDSM 300
QY      301  KCERVGVLSCHDNRVSCLGVTADGMAVATGSWDSFLKIWN 340
Db      301  RQERAGVLAGHDNRVSCLGVTEDGMAVCTGSWDSFLKIWN 340

RESULT 11
GBB2_RAT
ID      GBB2_RAT      STANDARD;      PRT;      340 AA.
AC      P54313;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      01-OCT-2000 (Rel. 40, Last annotation update)
DE      GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 2
DE      (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT).
GN      GNB2.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      [1]
RP      NCBL_TaxID=10116;
RR      SEQUENCE FROM N.A.
RC      STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA      Kuroda S., Tokunaga C., Konishi H., Kikkawa U.;
RL      Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC      INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC      SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC      GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC      EFFECTOR INTERACTION.
CC      -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC      -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U34959; AAC72248.1; -.
DR      HSSP; P04901; ITBG.
DR      InterPro; IPR001632; -.
DR      InterPro; IPR001680; -.
DR      Pfam; PF00400; WD40; 7.
DR      PRINTS; PR00319; GPROTEINB.

```

DR	PROSITE, PS00678; WD_REPEATS_1;	WD_REPEATS_1; 3.
DR	PROSITE; PS50082; WD_REPEATS_2; 6.	
KW	Transducer; Repeat; WD_REPEATS_REGION; 1.	
FT	REPEAT 53	WD 1.
FT	REPEAT 95	WD 2.
FT	REPEAT 141	WD 3.
FT	REPEAT 182	WD 4.
FT	REPEAT 224	WD 5.
FT	REPEAT 268	WD 6.
FT	REPEAT 310	WD 7.
SO	SEQUENCE	

SEQUENCE 340 AA; 37500 MW; 1A60E2755C5B71BB CRC64

Query Match 82.6%; Score 1495; DB 1; Length 340;
 Best Local Similarity 79.4%; Pred. No. 8.1e-124;
 Matches 270; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

QY 1 MGEMQLKQAEQLKKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
 1 MSELQKQAEQLKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
 DB 1 MSELQKQAEQLKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
 QY 61 MHVATDSKLLVASODGKLIWDTYTNKVAHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 61 MHVATDSKLLVASODGKLIWDTYTNKVAHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 DB 61 MHVATDSKLLVASODGKLIWDTYTNKVAHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 QY 121 CSYSLKREGNKKVRELTAHTGYLSCRFDDNNIVTSSGDTTCALMDIETGQOKTVF 180
 121 CSYSLKREGNKKVRELTAHTGYLSCRFDDNNIVTSSGDTTCALMDIETGQOKTVF 180
 DB 121 CSYSLKREGNKKVRELTAHTGYLSCRFDDNNIVTSSGDTTCALMDIETGQOKTVF 180
 QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQTFGHSIDINAICTFPNGEA 240
 181 VGHGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQTFGHSIDINAICTFPNGEA 240
 DB 181 VGHGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQTFGHSIDINAICTFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 300
 241 ICTGSDASCRLFDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 300
 DB 241 ICTGSDASCRLFDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 300
 QY 301 KCERGVLSGHDNRVSCIGVTADGMAVATGWSDFLKIWN 340
 301 KCERGVLSGHDNRVSCIGVTADGMAVATGWSDFLKIWN 340
 DB 301 KCERGVLSGHDNRVSCIGVTADGMAVATGWSDFLKIWN 340

RESULT 12
 GBB4_MOUSE STANDARD; PRT; 340 AA.
 AC P29387;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA
 CHAIN 4).
 GN GNB4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92181467; PubMed=1543505;
 RA von Weizsaecker E., Strathmann M.P., Simon M.I.;
 RT "Diversity among the beta subunits of heterotrimeric GTP-binding
 RT proteins: characterization of a novel beta-subunit cDNA.";
 RL Biochem. Biophys. Res. Commun. 183:350-356(1992).
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: S86124; AAB21609.1; -
 CC EMBL: M87286; AAA37756.1; -
 CC EMBL: M63658; AAA37664.1; -
 CC PIR: JS0669; RGMGB4.
 CC HSSP: P04901; ITBG.

DR MGD; MGI:104581; Gnb4.
 DR InterPro; IPR001632; -
 DR InterPro; IPR001680; -
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS0082; WD_REPEATS_2; 6.
 DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37354 MW; B21EBB29BA62B1E CRC64;

Query Match 82.5%; Score 1493; DB 1; Length 340;
 Best Local Similarity 79.1%; Pred. No. 1.2e-123;
 Matches 269; Conservative 37; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGEMQLKQAEQLKKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
 1 MSELQKQAEQLKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
 DB 1 MSELQKQAEQLKQIADARKACADITLAEVSGLEVGRVQMRTRRLRGLAKIYA 60
 QY 61 MHVATDSKLLVASODGKLIWDTYTNKVAHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 61 MHVATDSKLLVASODGKLIWDTYTNKVAHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 DB 61 MHVATDSKLLVASODGKLIWDTYTNKVAHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 QY 121 CSYSLKREGNKKVRELTAHTGYLSCRFDDNNIVTSSGDTTCALMDIETGQOKTVF 180
 121 CSYSLKREGNKKVRELTAHTGYLSCRFDDNNIVTSSGDTTCALMDIETGQOKTVF 180
 DB 121 CSYSLKREGNKKVRELTAHTGYLSCRFDDNNIVTSSGDTTCALMDIETGQOKTVF 180
 QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQTFGHSIDINAICTFPNGEA 240
 181 VGHGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQTFGHSIDINAICTFPNGEA 240
 DB 181 VGHGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQTFGHSIDINAICTFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 300
 241 ICTGSDASCRLFDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 300
 DB 241 ICTGSDASCRLFDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 300
 QY 301 KCERGVLSGHDNRVSCIGVTADGMAVATGWSDFLKIWN 340
 301 KCERGVLSGHDNRVSCIGVTADGMAVATGWSDFLKIWN 340
 DB 301 KCERGVLSGHDNRVSCIGVTADGMAVATGWSDFLKIWN 340

RESULT 13
 GBB_LYMST STANDARD; PRT; 341 AA.
 AC Q08706;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.
 OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Lymnaea.
 OX NCBI_TaxID=6523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CNS;
 RX MEDLINE=94242793; PubMed=7514444;
 RA Knol J.C., Roovers E., van Kesteren E.R., Planta R.J.,
 RA Vreugdenhil R., van Heerikhuizen H.;
 RT "A G-protein beta subunit that is expressed in the central nervous
 RT system of the mollusc Lymnaea stagnalis identified through cDNA
 RT cloning.";
 RL Biochim. Biophys. Acta 1222:129-133(1994).
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE

```
CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC EFFECTOR INTERACTION.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outpost at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; Z23105; CAA80652.1; -.
DR HSP; P04901; IGP2.
DR InterPro; IPR001632; -.
DR InterPro; IPR001680; -.
DR pfam; PF00400; WD40; 7.
DR PRINTS; PR00319; GPSTEINB.
DR PRINTS; PR00320; GPSTEINBRPT.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 5.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Transducer; Repeat; WD repeat.
FT REPEAT 54 84 WD 1.
FT REPEAT 96 126 WD 2.
FT REPEAT 142 171 WD 3.
FT REPEAT 183 213 WD 4.
FT REPEAT 225 255 WD 5.
FT REPEAT 269 299 WD 6.
FT REPEAT 311 341 WD 7.
SQ SEQUENCE 341 AA; 37320 MW; 4A2662588387592E CRC64;
```

Query Match	81.9%;	Score 1482;	DB 1;	Length 341;
Best Local Similarity	80.2%;	Pred. NO. 1.1e-122;		
Matches 271;	Conservative 29;	Mismatches 38;	Indels 0;	Gaps 0;

[illegible]

GN GBETA1.
OS Homarus americanus (American lobster).
OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98410740; PubMed=9740024;
RA Xu F., Hollins B., Landers T.M., McClintock T.S.;
RT "Molecular cloning of a lobster Gbeta subunit and Gbeta expression in
RT olfactory receptor neuron dendrites and brain neuropil."
RL J. Neurobiol. 36:525-536(1998).
CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC EFFECTOR INTERACTION.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

```

DR   InterPro; IPR001632; -
DR   InterPro; IPR001680; -
DR   Pfam; PF00400; WD40; 7.
DR   PRINTS; PR00319; GPROTEINB.
DR   PRINTS; PR00320; GPROTEINBPT.
DR   PROSITE; PS00678; WD_REPEATS_1; 3.
DR   PROSITE; PS50082; WD_REPEATS_2; 6.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW   Transducer; Repeat; WD repeat; Multigene family.
FT   REPEAT      53      83      WD 1.
FT   REPEAT      95      125     WD 2.
FT   REPEAT     141      170     WD 3.
FT   REPEAT     182      212     WD 4.
FT   REPEAT     224      254     WD 5.
FT   REPEAT     268      298     WD 6.
FT   REPEAT     310      340     WD 7.
SQ   SEQUENCE      340 AA;  37409 MW;  3483245F9291D82E CRC64;

```

Query Match	81.6%;	Score 1477;	DB 1;	Length 340;
Best Local Similarity	78.2%;	Pred. No. 3e-122;		
Matches 266;	Conservative 35;	Mismatches 39;	Indels 0;	Gaps 0;

OY		1	MGEMEQLKQEAQBQLKQIADARKACADITLAEVLVSGLEVGRVOMRTTRTLRGHLAKIYA	60
Dd		1	MNDLDLSRQEAEELKNTRIARKNALDFTLVQATAGMDPIGRIO MRTRTLRLGHIAKIYA	60
OY		61	MHWATDSKLVSASQDGKLIWMDTYTNNKVHAIPLRSSWMTCAYAPSGNFVACGGIDNM	120
Dd		61	MHWGSDSRNLVSASQDGKLIWMSDYTNKKVHAIPLRSSWMTCAYAPSGSYVACGGIDNI	120
OY		121	CSIYSLKSRREGNAVKSREL SAHTGYLSCCRFLDDNNTIVTS SGGDTLCALWDIETGOOKTVF	180
Dd		121	CSISYLKTREGNVAVSRELPGHTGYLSCCRFVDNQIVTSSCGMTCALWDIETGOOCTQF	180
OY		181	VGHTGDCMSLA VSPDYKLFISGACDASAKLMDVREGTCRQTFEGHESDINAI CFFPNGEA	240
Dd		181	TGHTGDVMSLSLSPMNRITFTSGACDASAKLMDIRDMCQRQTFEGHESDINAVTFFPNGBA	240
OY		241	ICTGSDDASCRLFELRADQELTAYSHE SII CGITSVA FSLSGRIIFLAGYDDFN CNVMSDL	300
Dd		241	FATGSDDATCRLEFDIRADQELAMYSHDNIICGITSVA FSKSGKILLAGYDDFN CNVMSDM	300

QY 301 KCERVGLSGHDNRVSCLGVTADGMAVATGWSDFLKIWN 340
 Db 301 RTERAGVLACHDNRVSCLGVTEDGMAVATGWSDFLKIWN 340

RESULT 15
 GBB2_BOVIN

ID GBB2_BOVIN STANDARD; PRT; 326 AA.

AC P11017;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 2
 DE (TRANSDUCIN BETA CHAIN 2). (G PROTEIN BETA 2 SUBUNIT) (FRAGMENT).
 GN GNB2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87231903; PubMed=3108879;
 RA Fong H.K.W., Amatruda T.T. III, Birren B.W., Simon M.I.;
 RT "Distinct forms of the beta subunit of GTP-binding regulatory
 RL proteins identified by molecular cloning.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3792-3796(1987).
 RN [2]

RP SEQUENCE OF 88-302 FROM N.A.
 RX MEDLINE=87317607; PubMed=3114742;
 RA Gao B., Gilman A.G., Robishaw J.D.;
 RT "A second form of the beta subunit of signal-transducing G proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6122-6125(1987).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; M16480; AAA30553.1; -;
 DR EMBL; M36431; AAA62717.1; -;
 DR EMBL; M16539; AAA30552.1; -;
 DR PIR; A26617; RGOB02.
 DR HSSP; P04901; IGP2.
 DR InterPro: IPR001680; -;
 DR Pfam; PF00400; WD40; 7.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT NON_TER 1
 FT REPEAT 39
 FT REPEAT 81
 FT REPEAT 127
 FT REPEAT 168
 FT REPEAT 210
 FT REPEAT 254
 FT REPEAT 296
 FT REPEAT 271
 FT CONFLICT 271
 SQ SEQUENCE 326 AA; 35645 MW; EE9B0EF5BCC51B23 CRC64;

Query Match 81.1%; Score 1467; DB 1; Length 326;

Best local Similarity 81.0%; Pred. No. 2, 2e-121;
 Matches 264; Conservative 29; Mismatches 33; Indels 0; Gaps 0;

QY 15 KKQIADARKACADITLAEVSGLEVGVQVQMRTRTLRGLAKIYAMHWATDSKLVAS 74
 Db 1 RNQIRDARKACAGDSTLFGITAGLDVPVGRIOQMRTRTLRGLAKIYAMHWATDSKLVAS 60
 QY 75 QDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNMCISYLSKREGNVK 134
 Db 61 QDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNMCISYLSKREGNVK 120
 QY 135 VSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQOKTVEVGHGTGDCMSLAVSP 194
 Db 121 VSRELPGHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQOKTVEVGHGTGDCMSLAVSP 180
 QY 195 DYKLFISGACDASAKLMDVREGTCRQTFTHESDINAICFPNGEALICTGSDASCRFLD 254
 Db 181 DGRFVSGACDASIKLMDVDSMCRQTFTHESDINAVAFEPNGYAFTTGSDATCRFLD 240
 QY 255 LRADQELTAYSHESIICGITSVAFSLSGRLLEAGYDDFNQVWDSLKCEVGLSGHDNR 314
 Db 241 LRADQELTAYSHDNIICGITSVAFSLSGRLLEAGYDDFNQVWDSLKCEVGLSGHDNR 300
 QY 315 VSCLGVTADGMAVATGWSDFLKIWN 340
 Db 301 VSCLGVTDDGMAVATGWSDFLKIWN 326

Search completed: September 28, 2001, 10:34:28
 Job time: 283 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:29:25 ; Search time 38.04 Seconds
(without alignments)
1182.537 Million cell updates/sec

Title: US-09-492-029-3
Perfect score: 1809
Sequence: 1 MGEMEQLEKQAEQLEKQIAD.....TADGMVATGSDSFLKIWN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues 425026

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: SP_TREMBL_16:*
 - 2: SP_archaea:*
 - 3: SP_bacteria:*
 - 4: SP_fungi:*
 - 5: SP_human:*
 - 6: SP_invertebrate:*
 - 7: SP_mammal:*
 - 8: SP_mhc:*
 - 9: SP_organellar:*
 - 10: SP_phage:*
 - 11: SP_plant:*
 - 12: SP_rodent:*
 - 13: SP_unclassified:*
 - 14: SP_vertebrate:*
 - 15: SP_virus:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1670	92.3	340	13	Q9DFG9	Q9dfg9 ambystoma t
2	1570	86.8	340	13	Q9DFH0	Q9dfh0 ambystoma t
3	1558	86.1	340	11	Q9QMG8	Q9qmg8 rattus norv
4	1506	83.3	340	11	Q9HAV0	Q9hav0 homo sapien
5	1496	82.7	340	4	Q9JHX8	Q9jhx8 mus musculu
6	1253	69.3	352	3	Q93887	Q93887 cryptococcu
7	1225.5	67.7	347	3	Q9HFS3	Q9hfs3 pneumocysti
8	1215.5	67.2	358	3	Q74214	Q74214 emericeila
9	957.5	52.9	352	5	Q9W3J1	Q9w3j1 drosophila
10	946.5	52.3	395	4	Q9HAU9	Q9haug homo sapien
11	830	45.9	346	5	Q9NFZ1	Q9nfz1 calliphora
12	826.5	45.7	377	10	Q9XFK0	Q9xfk0 pisum sativ
13	823.5	45.5	377	10	Q9SW94	Q9sw94 pisum sativ
14	823	45.5	346	5	Q9VW29	Q9vw29 drosophila
15	811	44.8	377	10	Q9FV61	Q9fv61 nicotiana t
16	794	43.9	380	4	Q64944	Q64944 avena fatua
17	739.5	40.9	283	4	Q9UFT3	Q9uft3 homo sapien
18	696.5	38.5	436	3	Q9Y7B8	Q9y7b8 kluyveromyc
19	689	38.1	186	5	O45041	O45041 homarus ame

20	637	35.2	371	5	Q9XZV6	Q9xzv6 geodia cydo
21	601	33.2	123	11	Q61621	Q61621 mus musculu
22	592.5	32.8	240	10	Q40456	Q40456 nicotiana t
23	313	17.3	1241	2	Q9XBD8	Q9xbd8 amycolatops
24	312	17.2	522	4	Q43445	Q43445 homo sapien
25	310	17.1	1049	2	Q9ZEM4	Q9zem4 streptomyc
26	310	17.1	1676	2	Q9KXX9	Q9kxx9 dictyosteli
27	309	17.1	579	5	Q76734	Q76734 dictyosteli
28	308.5	17.1	485	4	Q9NVX2	Q9nvx2 homo sapien
29	308	17.0	333	10	Q9SV00	Q9sv00 arabidopsis
30	308	17.0	520	4	Q43864	Q43864 homo sapien
31	305	16.9	502	3	Q74855	Q74855 schizosacch
32	305	16.9	521	4	Q43172	Q43172 homo sapien
33	299	16.5	473	10	Q9FLX9	Q9flx9 arabidopsis
34	295.5	16.3	561	3	Q14432	Q14432 schizosacch
35	295.5	16.3	586	3	Q9UUG8	Q9uug8 schizosacch
36	295	16.3	334	4	Q9NMW7	Q9nmw7 homo sapien
37	291.5	16.1	476	13	Q93531	Q93531 xenopus lae
38	288.5	15.9	318	5	Q96653	Q96653 trypanosoma
39	286.5	15.8	317	13	Q9W711	Q9w711 xenopus lae
40	285.5	15.8	481	5	Q9VPR4	Q9vpr4 drosophila
41	284	15.7	553	5	Q9VVT0	Q9vv10 drosophila
42	284	15.7	587	5	Q44083	Q44083 caenorhabdi
43	283.5	15.7	391	5	Q9VU65	Q9vu65 drosophila
44	282.5	15.6	613	10	Q9FNI9	Q9fni9 arabidopsis
45	281.5	15.6	480	5	Q96995	Q96995 drosophila

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	340 AA.
Q9DFG9	Q9DFG9			
AC	Q9DFG9			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	G-PROTEIN B3 SUBUNIT.			
OS	Ambystoma tigrinum (Tiger salamander).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Caudata; Salamandroldea; Ambystomatidae;			
OC	Ambystoma.			
OX	NCBI_TaxID=8305;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=RETINA;			
RA	Ryan J.C., Crouch R.K., Ma J.;			
RT	"Cloning and Characterization of G-protein Beta subunits from the			
RT	Salamander Retina."			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF277162; AAG31061.1; ..			
SQ	SEQUENCE 340 AA; 37355 MW; 6C284C1100552DBE CRC64;			

Query Match	92.3%;	Score 1670;	DB 13;	Length 340;	
Best local Similarity	88.8%;	Pred. No. 3,1e-145;			
Matches 302;	Conservative 25;	Mismatches 13;	Indels 0;	Gaps	
QY	1	MGEMEQLEKQAEQLEKQIADARKACADITLAEVSGLEVYGRVQMRTRRLRGLAKIYA	60		
DB	1	MGEMEQLEKQAEQLEKQIADARKACADITLAEVSGLEVYGRVQMRTRRLRGLAKIYA	60		
QY	61	MHWATDSKLIVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAIAPSGNFVACGLDNN	120		
DB	61	MHWATDSKLIVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAIAPSGNFVACGLDNN	120		
QY	121	CSIYSLKSRREGNVKVSRELSTHTGYLSCCFDDNNIVTSSGDTTCALMDIETGQKTVF	180		
DB	121	CSIYSLKSRREGNVKVSRELSTHTGYLSCCFDDNNIVTSSGDTTCALMDIETGQKTVF	180		
QY	181	VGHTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACIFPNGEA	240		
DB	181	VGHTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINACIFPNGEA	240		

Db 181 MGTGDCMSLAVSPDFRIFVSGACDATAKLMDIREGTCROTFTGHESDINAIICFPNGEA 240
QY 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFLSGRLLFAGYDDFNCNVWDSL 300
Db 241 VCTGSDATCRLFDLRADQELTAYSHESIICGITSVAFLSGRLLFAGYDDFNCNVWDSL 300
QY 301 KCERVGVLGSHDNRYSCLGVTADGMAVATGSDSFLKIWN 340
Db 301 KGERVGVLGSHDNRYSCLGVTADGMAVATGSDSFLKIWN 340

RESULT 2

Q9DFH0 PRELIMINARY; PRT; 340 AA.
AC Q9DFH0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
OS Ambystoma tigrinum (Tiger salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomidae;
OX NCBI_TaxID=8305;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RA Ryan J.C., Crouch R.K., Ma J.;
RT "Cloning and Characterization of G-protein Beta subunits from the
RL Salamander Retina."
DR Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
SQ EMBL: AF277161; AAG31060.1; -
SEQUENCE 340 AA; 37332 MW; 84E1451FDD83D8F3 CRC64;

Query Match
Best Local Similarity 86.8%; Score 1570; DB 13; Length 340;
Matches 282; Conservative 30; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGEMEOLKQEAOLKQIADARACADITLAEVSGLEVGRVQMRTRTLRGLAKIYA 60
Db 1 MSELQDLRQEAOLKQIADARACADITLAEVSGLEVGRVQMRTRTLRGLAKIYA 60
QY 61 MHMGTDSRLVSAQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
Db 61 MHMGTDSRLVSAQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSYSLKSRGNVKSRELTAHTGYLSCRFDDNNITVSSGDTTCALMDIETGQQTVE 180
Db 121 CSYSLKSRGNVKSRELTAHTGYLSCRFDDNNITVSSGDTTCALMDIETGQQTVE 180
QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
Db 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
QY 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFLSGRLLFAGYDDFNCNVWDSL 300
Db 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFLSGRLLFAGYDDFNCNVWDSL 300
QY 301 KCERVGVLGSHDNRYSCLGVTADGMAVATGSDSFLKIWN 340
Db 301 KCERVGVLGSHDNRYSCLGVTADGMAVATGSDSFLKIWN 340

RESULT 3

Q9QWG8 PRELIMINARY; PRT; 340 AA.
AC Q9QWG8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
RN G PROTEIN BETA SUBUNIT.
RG1.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Wang X.B., Funada M., Imai Y., Revey R.S., Ujike H., Vandenbergh D.J.,
RT "Rgl: A psychostimulant-regulated gene essential for establishing
RL cocaine sensitization."
DR EMBL: U88324; AAD00650.1; -
DR HSSP; P04901; 1TBG.
DR InterPro; IPR001632; -
DR InterPro; IPR001680; -
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00319; GPROTEINB.
DR PRINTS; PR00320; GPROTEINB.
DR PROSITE; PS00678; WD_REPEATS.
DR SMART; SM00320; WD40; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 340 AA; 37387 MW; D9EBEC6B0FF7EC57 CRC64;

Query Match
Best Local Similarity 86.1%; Score 1558; DB 11; Length 340;
Matches 280; Conservative 30; Mismatches 30; Indels 0; Gaps 0;

QY 1 MGEMEOLKQEAOLKQIADARACADITLAEVSGLEVGRVQMRTRTLRGLAKIYA 60
Db 1 MSELQDLRQEAOLKQIADARACADITLAEVSGLEVGRVQMRTRTLRGLAKIYA 60
QY 61 MHMGTDSRLVSAQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
Db 61 MHMGTDSRLVSAQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSYSLKSRGNVKSRELTAHTGYLSCRFDDNNITVSSGDTTCALMDIETGQQTVE 180
Db 121 CSYSLKSRGNVKSRELTAHTGYLSCRFDDNNITVSSGDTTCALMDIETGQQTVE 180
QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
Db 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
QY 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFLSGRLLFAGYDDFNCNVWDSL 300
Db 241 ICTGSDASCRLFDLRADQELTAYSHESIICGITSVAFLSGRLLFAGYDDFNCNVWDSL 300
QY 301 KCERVGVLGSHDNRYSCLGVTADGMAVATGSDSFLKIWN 340
Db 301 KCERVGVLGSHDNRYSCLGVTADGMAVATGSDSFLKIWN 340

RESULT 4

Q9HAV0 PRELIMINARY; PRT; 340 AA.
AC Q9HAV0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
OS GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT 4.
GN GNB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT "Cloning and Characterization of Human G-Protein Beta 4."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF300648; AAG18442.1; -

Db 252 AFATGSDASCKLFDLRADRELNSYAHNNILCGITSVAFSISGRVLFAGYDDYCNVMDT 311
QY 300 LKCEYGVLSGHDNRVSCIGVTADGMAVATGSDSFLKIWN 340
Db 312 LKGERIGVLAGHENRVSCMGVSGDVALCTGSDSLKVM 352

RESULT 7
Q9HFS3 PRELIMINARY; PRT; 347 AA.
AC Q9HFS3:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RA Puri V., Park J.G., Limper A.H., Thomas C.F. Jr.;
RT "The Pneumocystis carinii guanine nucleotide-binding protein beta
RT subunit";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
SR EMBL: AF306565; AAC27720.1; -
SQ SEQUENCE 347 AA; 38438 MW; FEE1495006E24882 CRC64;

Query Match 67.7%; Score 1225.5; DB 3; Length 347;
Best Local Similarity 66.9%; Pred. No. 2e-104;
Matches 222; Conservative 44; Mismatches 65; Indels 1; Gaps 1;

QY 9 QEAQLKQIADARKACADITLAEVSGLEVGRVQMTTRTLRGHLAKIYAMHWATDSK 68
Db 15 KEAEYLKEIKKKKDELADTLNLSMAQTLVDIERLSIRVRYTLKGLAKIYAMHWSTDOK 74
QY 69 LVSASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDMNCISYLSKS 128
Db 75 HLVSASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDMNCISYLSKS 134
QY 129 REGNVKVSRELTAHTGYLSCRELDNNIVTSSGDTTCALMDIETGQKTFVGHGTGDCM 188
Db 135 KDGHAKIARELMAHTGYLSCRELDNNIVTSSGDTTCALMDIETGQKTFVGHGTGDCM 194
QY 189 SLAVSP-DYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEAICTGSD 247
Db 195 SLVHPTNPNLFVSGACAFAKIWDIRIGKSVQTFAGHESDINAVQYFPNGNAFATGSD 254
QY 248 ASCRLFDLRADQELTAYSHESIICGITSVAFSLGRLLFAGYDDFNCNVWDSLKCEYGV 307
Db 255 ASCRLFDVRADRELNOYSAANIMCGITSISFSNGRLLFAGYDDFNCNVWDSLKCEYGV 314
QY 308 LSGHDNRVSCIGVTADGMAVATGSDSFLKIWN 339
Db 315 LQGHDRVSCVSGVSKDGRSLATGSDSLKIWN 346

RESULT 8
Q74214 PRELIMINARY; PRT; 352 AA.
AC Q74214:
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE G-PROTEIN BETA SUBUNIT.
OS Emeritella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emeritella.
OX NCBI_TaxID=5072;
RN [1]

RP SEQUENCE FROM N.A.
RA Rosen S., Yu J.-H., Adams T.H.;
RT "Aspergillus nidulans flba suppressor sfad identifies the G-beta
RT subunit of a heterotrimeric G protein."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF056182; AAC33436.1; -
DR HSSP; P04901; 1TBG.
DR InterPro; IPR001632; -
DR InterPro; IPR001680; -
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00319; GPROTEINB.
DR PRINTS; PR00320; GPROTEINBPT.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
DR SMART; SM00320; WD40; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 352 AA; 38888 MW; 186A16886B4DF466 CRC64;

Query Match 67.2%; Score 1215.5; DB 3; Length 352;
Best Local Similarity 64.6%; Pred. No. 1.7e-103;
Matches 223; Conservative 48; Mismatches 67; Indels 7; Gaps 3;

QY 2 GEMEQLK-----QEAQLKQIADARKACADITLAEVSG-LEVGRVQMTTRTLRGHL 55
Db 6 GEOMQAKITAAAREAEGLKDKIRRRKDDLADTLRDVAQNGQDALPRIGMKPRFTLKHL 65
QY 56 AKIYAMHWATDSKLLVSASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACG 115
Db 66 AKIYAMHWSTDRHLVSASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACG 125
QY 116 GLDNNCISYLSKREGNVKVSRELTAHTGYLSCRELDNNIVTSSGDTTCALMDIETGQ 175
Db 126 GLDNNCISYLSKREGNVKVSRELTAHTGYLSCRELDNNIVTSSGDTTCALMDIETGQ 185
QY 176 QKTVEFGHTGDCMSLAVSP-DYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICF 234
Db 186 KVTEFADHFGDVMSISINPTNQNIFVSGACDAFAKLMIDIRTKAVQTFAGHESDINAICF 245
QY 235 FPNGEAICTGSDASCRFLDLRADQELTAYSHESIICGITSVAFSLGRLLFAGYDDFNC 294
Db 246 FPDGNAFGTGSDDTCTCLFDIRADRSINTYQSDQILCGITSVGFVSGRLLFAGYDDFEC 305
QY 295 NWDLSKCEYGVLSGHDNRVSCIGVTADGMAVATGSDSFLKIWN 339
Db 306 KVMVDLGRGKRVGSLSGHENRVSCIGVSNDSISLCTGSDSFLKIWN 350

RESULT 9
Q9W3J1 PRELIMINARY; PRT; 358 AA.
AC Q9W3J1:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CG10763 PROTEIN.
GN CG10763.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlshina N.V., Mody B., Mody B., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003443; AAF46336.1; -.
 DR HSSP; P04901; 1TBG.
 DR FlyBase; FBgn0030011; CG10763.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS; 3.
 DR SMART; SM00320; WD40; 1.
 DR Repeat; WD repeat.
 SO SEQUENCE 358 AA; 39354 MW; E9C6DEF91C503231 CRC64;

Query Match 52.9%; Score 957.5; DB 5; Length 358;
 Best Local Similarity 49.1%; Pred. No. 8.3e-80;
 Matches 167; Conservative 78; Mismatches 92; Indels 3; Gaps 2;

QY 3 EMEQLKQAEQLKQIADARKACADITLAEVLVSGLEVGRVQMTTRTLRGHLAKIYAMH 62
 DB 18 KMASLVREANLKTLEERQKLDVNLNIAERLEQIAVNIKPRKVLKQKAVLCTD 77
 QY 63 WATDSKLVASASQDGLIWDITTTNKVHAIPLRSSWVMTCAVAPSGNEFVACGLDNMCS 122
 DB 78 WSPDKRHITISSQDGLIWDITTTNKVHAIPLRSSWVMTCAVAPSGNEFVACGLDNMCS 137
 QY 123 IYSLKSRGNVKSRELSAHTGYLSCCRFLD-DNNITVSSGDTTCALMDIETGQKTVFV 181
 DB 138 VYPTSDDEMAAKKRYVGFHTSYMSCICYPNSDQILITGSGDSTCALMDVESGQLLSFH 197
 QY 182 GHTGCMSLAVSPDY-KLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGE 239
 DB 198 GHSGDVMAIDLAPNETGNTFVSGSCDRMAFIWMKSGHVQSEFGHSDVNSVKFHPGCD 257
 QY 240 AICTGSDASCRLEFLRADQELTAYSHESITGITSVAFLSGLRLFAGYDDFCNCNWDS 299
 DB 258 AATGSDSSCRLYDMADREVAVFAKESITFGVNSVDSESGRLFLFAGYNDYTNLMDT 317
 QY 300 LKCEYGVLSGHDNRVSCLGVTADGMAVATGSDSFLKIW 339
 DB 318 LKSERVCLLYGHENKVCVQVSPDGTALSTGSDWDTIRW 357

RESULT 10
 Q9HAU9
 ID Q9HAU9 PRELIMINARY; PRT; 395 AA.
 AC Q9HAU9;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT 5L.
 GN GNB5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Publ H.L. Ili, Ikeda S.R., Aronstam R.S.;
 RT "Cloning and characterization of human G-protein beta 5L subunit.";
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF300650; AAG18444.1; -.
 SO SEQUENCE 395 AA; 43566 MW; E001B07ECFA587AD CRC64;

Query Match 52.3%; Score 946.5; DB 4; Length 395;
 Best Local Similarity 51.9%; Pred. No. 9.6e-79;
 Matches 177; Conservative 56; Mismatches 103; Indels 5; Gaps 3;

QY 4 MEQLKQAEQLKQIADARKACADITLAEVLVSGLEVGRVQMTTRTLRGHLAKIYAMH 63
 DB 54 LASLKSEAESLKGKLEERAKLHDELHOVAERVEALGFVMTKTRTLKGHNKVLCDW 113
 QY 64 ATDSKLVASASQDGLIWDITTTNKVHAIPLRSSWVMTCAVAPSGNEFVACGLDNMCS 123
 DB 114 CKDKRRIVSSQDGLIWDITTTNKVHAIPLRSSWVMTCAVAPSGNEFVACGLDNMCS 173
 QY 124 YSL-KSREGNVAVSRELSAHTGYLSCCRFLD-DNNITVSSGDTTCALMDIETGQKTVF 180
 DB 174 YPLTFDKNENNAKKKSVAMHTNYSACSEFTNSDMQILITASGDTGTCALMDVESGQLLSF 233
 QY 181 VGHGTG--CMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNG 238
 DB 234 HGHGADVLCGLDLPSETGNTFVSGGCDKAMWDMRSGCQVQAFETHESDINSVRYPPSG 293
 QY 239 EAICTGSDASCRLEFLRADQELTAYSHESITGITSVAFLSGLRLFAGYDDFCNCNW 298
 DB 294 DAFASGSDATCRLYDLRADREVAIYSKESIIFGASSVDLSGLRLFAGYNDYTNW 353
 QY 299 SLKCEYGVLSGHDNRVSCLGVTADGMAVATGSDSFLKIW 339
 DB 354 VLKGSRAVSLFGHENRVSTLRVSPDGTAFCSGSDWDTIRW 394

RESULT 11
 Q9NFZ1
 ID Q9NFZ1 PRELIMINARY; PRT; 346 AA.
 AC Q9NFZ1;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.
 OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Calliphoridae; Calliphora.
 OX NCBI_TaxID=7373;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=eye;
 RC Tissue=eye;
 RA Schulz S., Huber A., Schwab K., Paulsen R.;
 RT "A novel gamma subunit of the fly compound eye.";
 RT protein gamma subunit of the fly compound eye.";
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ250442; CAB76452.1; -.
 DR InterPro; IPR000364; -.

DR InterPro; IPR001632; -
 DR InterPro; IPR001680; -
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PRO0319; GPROTEINB.
 DR PRINTS; PRO0320; GPROTEINB.
 DR PRODOM; PD004738; -; 1.
 DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
 DR Repeat; WD repeat.
 KW Repeat; WD repeat.
 SQ SEQUENCE 346 AA; 38383 MW; 0C88F33C518FAE55 CRC64;

Query Match 45.9%; Score 830; DB 5; Length 346;
 Best Local Similarity 43.7%; Pred. No. 4e-68;
 Matches 148; Conservative 78; Mismatches 111; Indels 2; Gaps 1;

QY 3 EMEOLKQEARQLKQIADARKACADITLAEVSGLEVGVQMTRTLRGLAKIYAMH 62
 Db 7 ETQKLYDEINGLIKFFODHKAKADCTMQEKGCGDMSDIPKIRLSKKILKHNKNSVH 66
 QY 63 WATDSKLVSASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNMCS 122
 Db 67 FAGDSRHCVTGSIDGKLIWDTWTANKVYIPLRSAWMTVAFSPSGNFVACGGLDNMCT 126
 QY 123 IYSLKSRE--GNVYVRELSAHTGYLSCCRFLDDNNITVSSGDTTCALMDIETGQOKTVE 180
 Db 127 YVDVNNRDASGVAKMTRELGLGEGFLSCRFLLDTHLITGSGDMKICHWDLKGVKTFMDF 186
 QY 181 VGHGTGDCMSLAVSPDYKFLISGACDASAKIMDVREGTCROTFTGHESDINAICFPNGEA 240
 Db 187 NGHAGDIAGLSLSPDMNTYITGSVDKTAKIMDVRETHKQMEFGHEMDVNSVCYHPSGNG 246
 QY 241 ICTGSDDASCRLFDLRADQELTAYSHESITGITSVAFLSGLLFAGYDDFNCNWDLSL 300
 Db 247 FASASEDQTLRLYDIRADQIALYEPPOKNTGFTSCALSTSGRYLLCSGIEGNIHSFDTM 306
 QY 301 KCERYGVLSGHDNRVSCLEVTADGMAYATGWSDFLKIW 339
 Db 307 KVCCHNGMLQGHENRITCISLSPNGMCLASTSWDQVRLW 345

RESULT 12
 Q9XFK0 PRELIMINARY; PRT; 377 AA.
 AC Q9XFK0; 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE G PROTEIN BETA SUBUNIT.
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu Y., Tuteja N.;
 RT "Isolation and characterization of G protein from pea."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF145976; AAD33959.1; -
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001632; -
 DR InterPro; IPR001680; -
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PRO0319; GPROTEINB.
 DR PRINTS; PRO0320; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
 DR SMART; SM00320; WD40; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 377 AA; 40975 MW; B524084CABEB68C7 CRC64;

Query Match 45.7%; Score 826.5; DB 10; Length 377;
 Best Local Similarity 48.7%; Pred. No. 9.3e-68;

Matches 151; Conservative 71; Mismatches 69; Indels 19; Gaps 7;

QY 49 RFLRGLAKIYAMHWATDSKLVSASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPS 108
 Db 59 RFLQHTGKYSIDMTSEKNRIVSASQDGLIWNALTSQTHAIKLPICAWMTCAFSPT 118
 QY 109 GNFVACGGLDNMCSISLSK---REGNVYVRELSAHTGYLSCCRFL--DDNNITVSSGD 163
 Db 119 GQSVACGGLDSVCSIFNLNSPLDRDGNLNVSRMLSGHKGYVSCQYVPGEDTHLTGSGD 178
 QY 164 TTCALMDIETGQOKTVE-----GHTGDCMSLAVS-PDYKFLISGACDASAKIMDVREGT 217
 Db 179 QTCVLMWDTTGLRTSVFLGFEFQSGHTADVLSISNGSKLFEVSGSCDATALRLMDTRVAS 238
 QY 218 -CROTFTGHESDINAICFPNGEAICTGSDDASCRLFDLRADQELTAYS--HESIICGI 273
 Db 239 RAVRPFHGHGEGDVNSVKKFPDGNRFGTSGEDGCRLLFDIRTHQQLQVYNOQHODNEMAHV 298
 QY 274 TSVAFLSGLRLFAGYDDFNCNWDLSKCEV---GYLSGHDNRVSCLEVTADGMAYAT 329
 Db 299 TSIAFSISGRLLIAGTYNGCYWDTLLAKAVNLGSLQNSHGRITCLGMSADGSALCT 358
 QY 330 GSWDSFLKIW 339
 Db 359 GSWDTNLEKIW 368

RESULT 13
 Q9SW94 PRELIMINARY; PRT; 377 AA.
 ID Q9SW94;
 AC Q9SW94; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE G PROTEIN BETA SUBUNIT.
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ALASKA; TISSUE=APICAL BUD;
 RA Lapik Y.R., Kaufman L.S.;
 RT "Cloning of cDNA encoding pea G protein beta subunit."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF170921; AAD49742.1; -
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001632; -
 DR InterPro; IPR001680; -
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PRO0319; GPROTEINB.
 DR PRINTS; PRO0320; GPROTEINB.
 DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
 DR SMART; SM00320; WD40; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 377 AA; 40989 MW; F4744C8C4AA32B8B CRC64;

Query Match 45.5%; Score 823.5; DB 10; Length 377;
 Best Local Similarity 48.7%; Pred. No. 1.8e-67;
 Matches 151; Conservative 70; Mismatches 70; Indels 19; Gaps 7;

QY 49 RFLRGLAKIYAMHWATDSKLVSASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPS 108
 Db 59 RFLQHTGKYSIDMTSEKNRIVSASQDGLIWNALTSQTHAIKLPICAWMTCAFSPT 118
 QY 109 GNFVACGGLDNMCSISLSK---REGNVYVRELSAHTGYLSCCRFL--DDNNITVSSGD 163
 Db 119 GQSVACGGLDSVCSIFNLNSPLDRDGNLNVSRMLSGHKGYVSCQYVPGEDTHLTGSGD 178
 QY 164 TTCALMDIETGQOKTVE-----GHTGDCMSLAVS-PDYKFLISGACDASAKIMDVREGT 217
 Db 179 QTCVLMWDTTGLRTSVFLGFEFQSGHTADVLSISNGSKLFEVSGSCDATALRLMDTRVAS 238

Db 179 QTCVLMDITGLRTSVGEFGSGHADVLSISNGSKLFVSGSCDATALMDTRVAS 238
 QY 218 -CROTFTGHESDINAIKCEFPNGEALCTGSDASCRLEFDRADQELTAYS---HESITIGI 273
 Db 239 RAVRTFHGHEGVNSVKEFPDNGRFGTSGEDGTCLREDIRTGHLQVYNOQHDNEMAHV 298
 QY 274 TSVAFSLSGRLIFAGYDDFNQVWDSLKCEV---GVLGSHDNVSCIGVTADGMAVAT 329
 Db 299 TSIAFSTISGRLLIAGYTGNGCYWDTLLAKVNLGSLONSHEGRITCLGMSADGSAICT 358
 QY 330 GSWDSFLKIW 339
 Db 359 GSWDTNLIKIW 368

RESULT 14
 Q9VW29 PRELIMINARY; PRT; 346 AA.
 AC 09VW29; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE GBETA76C PROTEIN.
 GN G-BETA-76C OR GBETA76C OR CG8770.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.A., Butler J., Borkstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Chervy J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieri S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pacleb J.M.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.C.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003516; AAF49124.1;
 DR HSSP; P04901; 1TBG.

DR FlyBase; FBgn0004623; G-beta-76C.
 DR InterPro; IPR001632; -;
 DR InterPro; IPR001680; -;
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS; 1.
 DR SMART; SM00320; WD40; 1.
 KW Repeat; WD repeat.
 SO SEQUENCE 346 AA; 38335 MW; E9B22D937EC3A707 CRC64;

Query Match 45.5%; Score 823; DB 5; Length 346;
 Best Local Similarity 43.4%; Pred. No. 1.7e-67;
 Matches 147; Conservative 79; Mismatches 111; Indels 2; Gaps 1;

QY 3 EMBOLKQEAQKQIADARKACADITLAEVSGLEVGRVQMTTRTGLHAKIYAMH 62
 Db 7 ETQKLYDEINGMIOKFKDDQSKADCTLADKCGMDVDPKIRFSSKILKGHINKVSVH 66
 QY 63 WATDSKLVSASQDGLIWDITVTNKNVHAIPLRSSVMTCAVAPSGNVVACGLDNMCS 122
 Db 67 FAGDSRHCVTSLDGKLIIMDTWTANKVQIIPLRSAWMTVAFSPGNFVACGMDNCT 126
 QY 123 IYLSKSRE--GNVKSRELHAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQKTVF 180
 Db 127 VYDVNNRDSAGVAKMVKELMEYEGFLSSCRFLDDGHLITGSGDMKCHWDLKGVKTMDF 186
 QY 181 VGHGTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAIKCEFPNGEA 240
 Db 187 NGHAGDIAGLSLSPDMKTYITGSDVDTAKLMDVREGHKQMFQGHMDVSSVCYHPSGFG 246
 QY 241 ICTGSDDASCRLFLDRADQELTAYSHESTICGITSVAFSLSGRLIFAGYDDFNQVWDSL 300
 Db 247 FASCSQEDQATARMYDLRADQOIAQYEPQKNTGFTSCALSTSGRYLMCGIEGNVHSDTM 306
 QY 301 KCEKRVGLSGHDNRVSCLGVTADGMAVATGWSDFLKIW 339
 Db 307 KORHTGTLSGHEHRTICISLCPNGMCIASTSWDQVRLW 345

RESULT 15
 Q9FV61 PRELIMINARY; PRT; 377 AA.
 AC 09FV61; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE HETEROTRIMERIC GTP-BINDING PROTEIN SUBUNIT BETA 1.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Solanaceae; Nicotiana.
 OX NCBI_Taxid=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SAMSUN; TISSUE=HAIRY ROOT;
 RX MEDLINE=21002315; PubMed=11126570;
 RA Ando S., Takumi S., Ueda Y., Ueda T., Mori N., Nakamura C.,
 RT "Nicotiana tabacum cDNAs encoding alpha and beta subunits of a
 RT heterotrimeric GTP-binding protein isolated from hairy root tissues.";
 RL Genes Genet. Syst. 75:211-221(2000).
 DR EMBL; AF249743; AAG12330.1;
 SO SEQUENCE 377 AA; 40914 MW; 7052089F40A1707E CRC64;

Query Match 44.8%; Score 811; DB 10; Length 377;
 Best Local Similarity 45.1%; Pred. No. 2.5e-66;
 Matches 161; Conservative 71; Mismatches 99; Indels 26; Gaps 9;

QY 4 MEQLKQEAQKQIADARKACADITLAEVSGLEV--GRVQMTTRTGLHAKIYAM 61
 Db 17 VNDLREKLKQKRLQLD-----TDVSGYARSGQKTPVTFGPTDLVCCRILOGHGVKYSYL 71

Fri Sep 28 10:45:10 2001

us-09-492-029-3.rspt

Page 8

```
QY 62 HWATDSKLYSASODGKLYMDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNMC 121
   : |||||: |||: | | | | : |||||: ||| |||||: |
Db 72 DWTPEKNRIYASASODGRLIWNALTSQKTHAIKLPACAWMTCAFSPSGQSVACGGLD SVC 131
QY 122 SIYSLKS--REGNVKSRELSTHTCYLSCREFL--DDNNIVTSSGDTTCALWDIETGOQ 176
   ||:| | :|| | | | | | | | | | : | : ||||| | | | | | :
Db 132 SIFNLNSPIDKGNHVPVSRMLSGHKGIVSSCOYVPDEDTHLITSSGDQTCVIMDITTLR 191
QY 177 KTVF-----VGHGDCMSLAV-SPDYKLFISGACDASAKLMDVREGT-CROTFTGHESDI 229
   :|| | | | | | | | | | | | | | | | : || | | | | :
Db 192 TSVEGGEFQSGHTADYQSVSISSSNRPLFVSGSCDTTAGLMDYRVA SRAQRTPYGHG DY 251
QY 230 NAICFFPNGEALCTGSDDASCRLFDLRADQELTAYSH--ESTICGITSVAFSISGRLLF 286
   | : | | | | | | | | | | | | | | | : | : ||: |||: |||||
Db 252 NTVKFSPPDGNRFGTGSEDTCLRFDIRGTGHLQVYYQPHGDGDI PHVTSMAFSISGRLLF 311
QY 287 AGYDDFNCNVWDSLKCERY----GYLSGHDNRVSLGVTADGMAVATGSWDSFLKIW 339
   || : : | | | | | : | | : | : | | | | : || | | : ||||
Db 312 VGYSNGDCYVMDTLAKVYVNLGCVQNSHEGRISCLGLSADGSALCTGSMWDTNLKIW 368
```

Search completed: September 28, 2001, 10:34:06
Job time: 281 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:28:49 ; Search time 25.94 Seconds
(without alignments)
998.433 Million cell updates/sec

Title: US-09-492-029-3
Perfect score: 1809
Sequence: 1 MGEMEQLKQAEQOLKKQIAD.....TADGMAVATGSGWDSFLKIWN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1809	100.0	340	2	I53871	G-protein beta-sub
2	1762	97.4	340	1	RGHUB3	GTP-binding regula
3	1573	87.0	340	1	RGHUB1	GTP-binding regula
4	1573	87.0	340	1	RGBOB1	GTP-binding regula
5	1573	87.0	340	2	JC5057	G protein beta 1 -
6	1523	84.2	340	1	RGHUB2	GTP-binding regula
7	1520	84.0	340	2	T20830	hypothetical prote
8	1515	83.7	340	1	RGKWB	GTP-binding regula
9	1493	82.5	340	1	RGMSB4	GTP-binding regula
10	1482	81.9	341	2	S34348	GTP-binding regula
11	1467	81.1	326	1	RGOBE	GTP-binding regula
12	1467	81.1	341	1	RGFEBH	GTP-binding regula
13	1452	80.3	340	1	A47370	GTP-binding regula
14	1225	67.7	347	2	A54969	beta-5 GTP-binding
15	945.5	52.3	353	2	T22478	hypothetical prote
16	939.5	51.9	356	2	T03765	GTP-binding regula
17	844	46.7	380	2	T02085	GTP-binding protei
18	828	45.8	380	2	T07376	G-protein beta cha
19	827	45.7	377	2	RGFEB	GTP-binding regula
20	826	45.7	346	1	T03256	GTP-binding protei
21	826	45.7	375	2	T04086	GTP-binding protei
22	826	45.7	377	2	T04089	GTP-binding protei
23	825	45.6	377	2	T05266	GTP-binding regula
24	817	45.2	377	2	T08036	GTP-binding regula
25	794	43.9	380	2	T16985	GTP-binding protei
26	792	43.8	377	2	T17256	hypothetical prote
27	739.5	40.9	283	2	S72457	GTP-binding regula
28	664	36.7	317	2	T50474	GTP-binding regula
29	663	36.7	305	2		

30	635	35.1	423	2	S60939	GTP-binding protei
31	601	33.2	123	2	S29121	GTP-binding regula
32	592.5	32.8	240	2	T02059	GTP-binding regula
33	383.5	21.2	1356	2	T18521	beta transducin-1i
34	310	17.1	1049	2	T42045	probable WD-repeat
35	308	17.0	333	2	G85034	trp-asp repeat con
36	305.5	16.9	465	2	A32569	GTP-binding protei
37	305	16.9	502	2	T41148	GTP-binding protei
38	297.5	16.4	317	2	B33928	GTP-binding regula
39	297.5	16.4	317	2	S45054	GTP-binding regula
40	297.5	16.4	317	2	S38398	activated protein
41	297.5	16.4	317	2	A36986	WD-40 repeat regul
42	297.5	16.4	586	2	T38992	transcription init
43	295.5	16.3	704	2	S33263	probable U4/U6 sma
44	295	16.3				
45	294	16.3	554	2	T02445	

ALIGNMENTS

RESULT 1
I53871
G-protein beta-subunit - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C:Accession: I53871
R:Ray, K.; Robishaw, J.D.
Gene 149, 337-340, 1994
A:Title: Cloning and sequencing of a rat heart cDNA encoding a G-protein beta subunit
A:Reference number: I53871; MUID:95047499
A:Accession: I53871
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-340 <RES>
A:Cross-references: GB:L29090; NID:g456703; PIDN:AAA62620.1; PID:g456704
C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
F:222-255/Domain: WD repeat homology <WDR>

Query Match	100.0%	Score 1809	DB 2	Length 340
Best Local Similarity	100.0%	Pred. No. 2.2e-142		
Matches	340	Conservative	0	Mismatches 0; Indels 0; Gaps 0
QY	1	MGEMEQLKQAEQOLKKQIADARKACADITLAEVSGLEVGVQMRTRTLRGHAKIYA	60	
DB	1	MGEMEQLKQAEQOLKKQIADARKACADITLAEVSGLEVGVQMRTRTLRGHAKIYA	60	
QY	61	MHWATDSKLLVASASQDGKLIWDTYTTNKVHAIPLRSSWVMPCAYAPSGNFVACGGLDNN	120	
DB	61	MHWATDSKLLVASASQDGKLIWDTYTTNKVHAIPLRSSWVMPCAYAPSGNFVACGGLDNN	120	
QY	121	CSISLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQKTVF	180	
DB	121	CSISLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQKTVF	180	
QY	181	VGHTGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFTGHESDINAIICFPNGEA	240	
DB	181	VGHTGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCROTFTGHESDINAIICFPNGEA	240	
QY	241	ICTGSDPASCRLFDLRADQELTAISHESITICGITSVAFSLSGRLFAGYDDFNQVWDSL	300	
DB	241	ICTGSDPASCRLFDLRADQELTAISHESITICGITSVAFSLSGRLFAGYDDFNQVWDSL	300	
QY	301	KCERVGVLSGHDNRVSCIGVTADGMAVATGSGWDSFLKIWN	340	
DB	301	KCERVGVLSGHDNRVSCIGVTADGMAVATGSGWDSFLKIWN	340	

RESULT 2
RGHUB3
GTP-binding regulatory protein beta-3 chain - human
N:Alternate names: guanine nucleotide binding protein beta-3 chain; heterotrimeric G-

C/Species: Homo sapiens (man)
C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C/Accession: A35096
R/Levine, M.A.; Smallwood, P.M.; Moen Jr., P.T.; Helman, L.J.; Ahn, T.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 2329-2333, 1990
A/Title: Molecular cloning of beta3 subunit, a third form of the G protein beta-subunit
A/Reference number: A35096; MUID:90192801
A/Accession: A35096
A/Molecule type: mRNA
A/Residues: 1-340 <LEV>
A/Cross-references: GB:M31328; NID:g183412; PIDN:AAA52582.1; PID:g306776
C/Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
ains. The beta and gamma chains, required for GTPase activity, appear to be common to all
rase: It is specific for each type of G protein.
C/Comment: In mammals, four distinct types of beta chains have been found.
C/Genetics:

A;Gene: GDB:GNB3
A;Cross-references: GDB:120005; OMIM:139130
A;Map position: 12p13-12p13
C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C;Keywords: GTP binding; heterotrimer; signal transduction
F;51-84/Domain: WD repeat homology <WD1>
F;88-126/Domain: WD repeat homology <WD2>
F;139-171/Domain: WD repeat homology <WD3>
F;180-213/Domain: WD repeat homology <WD4>
F;222-255/Domain: WD repeat homology <WD5>
F;263-299/Domain: WD repeat homology <WD6>
F;308-340/Domain: WD repeat homology <WD7>

Query Match	.97.48;	Score 1762;	DB 1;	Length 340;
Best Local Similarity	96.5%;	Pred. No. 1.7e-138;		
Matches 328; Conservative	8;	Mismatches 4;	Indels 0;	Score 1762;

```
QY      1 MGENEQLKQAEQLKKQIADARKACADITLAEVSGLEVGRVQMRTTRTLRGLAKIYA    60
        |||||:|||||
Db      1 MGEMEQLROEAELKKQIADARKACADVTLAEVSGLEVGRVQMRTTRTLRGLAKIYA    60
QY      61 MHWATDSKLVSASODGKLIWDTYTTNKYHAIPLRSSWMTCAYAPSGNFVACGGLDNM   120
        |||||:|||||
Db      61 MHWATDSKLVSASODGKLIWDSYTINKYHAIPLRSSWMTCAYAPSGNFVACGGLDNM   120
QY      121 CSIYSLKSREGNAVYSRELSAHTGYLSRCRFLDDNNIVTSSGDTTCALWDIETGOOQTYF  180
        ||||:|||||
Db      121 CSIYNLKSRGNKVYSRELSAHTGYLSRCRFLDDNNIVTSSGDTTCALWDIETGOOQTYF  180
QY      181 VGHGTDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA   240
        |||||:|||||
Db      181 VGHTGDCMSLAVSPDENLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA   240
QY      241 ICTGSDDASCRLFDLRADOELTAVSHESIICGITSVAFSLGRLLFAGYDDPNCNVWDSL   300
        |||||:|||||
Db      241 ICTGSDDASCRLFDLRADOELTAVSHESIICGITSVAFSLGRLLFAGYDDPNCNVWDSL   300
QY      301 KCERVGVLSGHDNRVSCIGVTADGMVAATGWSDFEKIWN 340
        | ||||:|||||
Db      301 KSERVGILSGHDNRVSCIGVTADGMVAATGWSDFEKIWN 340
```

RESULT 3
RGHUB1
GTP-binding regulatory protein beta-1 chain - human
N/Alternate names: guanine nucleotide binding protein beta-1 chain; heterotrimeric G-protein
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C/Accession: A24853
R/Codina, J.; Stengel, D.; Woo, S.L.C.; Birnbaumer, L.
FEBS Lett. 207, 187-192, 1986
A/Title: Beta-subunits of the human liver Gs/Gi signal-transducing proteins and those of other tissues
A/Reference number: A91368; MUID:87030912
A/Accession: A24853
A/Molecule type: mRNA
A/Residues: 1-340 <COD>

A;Cross-references: GB:X04526; NID:g31667; PIDN:CA28207.1; PID:g31669
A;Experimental source: liver
A;Note: the authors translated the codon GAG for residues 138 and 172 as Glu
ains. The beta and gamma chains are a family of guanine nucleotide-binding proteins that re
rase; it is specific for each type of G protein.
C;Comment: In mammals, four distinct types of beta chains have been found.
C;Genetics:
A;Gene: GDB:GNB1
A;Cross-references: GDB:119279; OMIM:139380
A;Map position: 1p36-1p31.2
C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C;Keywords: GTP binding; heterotrimer; signal transduction
F;51-84/Domain: WD repeat homology <WD1>
F;88-126/Domain: WD repeat homology <WD2>
F;139-171/Domain: WD repeat homology <WD3>
F;180-213/Domain: WD repeat homology <WD4>
F;222-255/Domain: WD repeat homology <WD5>
F;263-299/Domain: WD repeat homology <WD6>
F;308-340/Domain: WD repeat homology <WD7>

Query Match	87.08;	Score 1573;	DB 1;	Length 340;
Best Local Similarity	83.28;	Pred. No. 7.9e-123;		
Matches 283;	Conservative 31;	Mismatches 26;	Indels 0;	Gaps 0

QY	1	MGEBOQLKQAEQOLKKOIALDARKACADITTLAEIVSGLEWVGRVOMRTTRTLRGHLAKIYA	60
Db	1	MSELDOLRQAEQOLKNOIRDARKACADATLSQTTNNIDPVGRIQMRTRTLRGHLAKIYA	60
QY	61	MHWATDSKLLVASASODGKLIWMDTYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM	120
Db	61	MHWGTD SRLVLVASASODGKLIWMDSYTTNKVHAIPLRSSWMTCAVAPSGNYVACGGLDNI	120
QY	121	CSISLKSREGNAVKSRELSAHTGYLSCCRFLDNNIIVTSSGDTTCALMDIETGQOKTYF	180
Db	121	CSITNLKTRREGNAVRSRELAGHTGYLSCCRFLDNNIIVTSSGDTTCALMDIETGQOQITTF	180
QY	181	VGHTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICEFPPNGEA	240
Db	181	TGHTGDVMSLSLAPDTRLFVSGACDASAKLMDVREGMCRQFTGHESDINAICEFPPNGNA	240
QY	241	ICTGSDDASCRLFDLRADQELTAVSHESIICGITSVAFLSGRLLFAGYDDFNCAWWSL	300
Db	241	FATGSDDATCRFLDLRADQELMTVSHDNIICGITSVSFSGRLLLAGYDDFNCAWWDAL	300
QY	301	KCERVGVI SGHDNRVSCIGVTADGMAVATGWSWDSFLK1WN 340	
Db	301	KADRAGYLAGHDNRVSCIGVTDDGMAVATGWSWDSFLK1WN 340	

RESULT 4
RGBOB1
GTP-binding regulatory protein beta-1 chain - bovine
N/Alternate names: guanine nucleotide binding protein beta-1 chain; heterotrimeric G-
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Dec-1992 #sequence
C/Accession: A24225; A25457
R/Sugimoto, K.; Nukada, T.; Tanabe, T.; Takahashi, H.; Noda, M.; Minamino, N.; Kangawa
FEBS Lett. 191, 235-240, 1985
A/Title: Primary structure of the beta-subunit of bovine transducin deduced from the
A/Reference number: A24225; MUID:86030675
A/Accession: A24225
A/Molecule type: mRNA
A/Residues: 1-340 <SUG>
A/Cross-references: GB:X03073
R/Fong, H.K.W.; Hurley, J.B.; Hopkins, R.S.; Miake-Lye, R.; Johnson, M.S.; Doolittle,
Proc. Natl. Acad. Sci. U.S.A. 83, 2162-2166, 1986
A/Title: Repetitive segmental structure of the transducin beta subunit: homology with
A/Reference number: A25457; MUID:86177563
A/Accession: A25457
A/Molecule type: mRNA
A/Residues: 1-340 <FON>

Query Match	87.0%;	Score 1573;	DB 1;	Length 340;
Best Local Similarity	83.2%;	Pred. No. 7.9e-123;		
Matches 283;	Conservative 31;	Mismatches 26;	Indels 0;	Gaps 0;

RESULT 5

Query Match	87.08;	Score 1573;	DB 2;	Length 340;
Best Local Similarity	83.28;	Pred. No. 7.9e-123;		

RESULT 6

RGHUB2
GTP-binding regulatory protein beta-2 chain - human
N;Alternate names: guanine nucleotide binding protein beta-2 chain; heterotrimeric G-
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: B26617; B28040
R;Fong, H.K.W.; Amatruda III, T.T.; Birren, B.W.; Simon, M.I.
Proc. Natl. Acad. Sci. U.S.A. 84, 3792-3796, 1987
A;Title: Distinct forms of the beta-subunit of GTP-binding regulatory proteins identi
A;Reference number: A94155; MUID:87231903
A;Accession: B26617
A;Molecule type: mRNA
A;Residues: 1-340 <FON>
A;Cross-references: GB:M16514; NID:g183469; PIDN:AAA03179.1; PID:g386751
R;Gao, B.; Gilman, A.G.; Robishaw, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6122-6125, 1987
A;Title: A second form of the beta subunit of signal-transducing G proteins.
A;Reference number: A94177; MUID:87317607
A;Accession: B28040
A;Molecule type: mRNA
A;Residues: 1-340 <GAO>
A;Cross-references: GB:M16538
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
ains. The beta and gamma chains, required for GTPase activity, appear to be common to
rase; it is specific for each type of G protein.
C;Comment: In mammals, four distinct types of beta chains have been found.
C;Genetics:
A;Gene: GDB:GNB2
A;Cross-references: GDB:120004; OMIM:139390
A;Map position: 7q21.3-7q22.1
C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C;Keywords: GTP binding; heterotrimer; signal transduction
F;51-84/Domain: WD repeat homology <WD1>
F;88-126/Domain: WD repeat homology <WD2>
F;139-171/Domain: WD repeat homology <WD3>
F;180-213/Domain: WD repeat homology <WD4>
F;222-255/Domain: WD repeat homology <WD5>
F;263-299/Domain: WD repeat homology <WD6>
F;308-340/Domain: WD repeat homology <WD7>

```

QY 1 MGEMQLKQEAQKQIADARACADITLAEVLGVEVGRVQMRTRRLRGLAKIYA 60
Db 1 MSELQDLKQEAQKQIADARACADITLAEVLGVEVGRVQMRTRRLRGLAKIYA 60
QY 61 MHMATDSKLLVASASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
Db 61 MHMTDSRLLVASASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSIYSLKSRGNVKSRELKSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQOKTVE 180
Db 121 CSIYSLKTRGNVKSRELKSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQOKTVE 180
QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
Db 181 AGHSGDVMSLSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
QY 241 ICTGSDDASCRLFLRADQELTAYSHESITGITSVAFLSGRLFAGYDDFNCNVWDSL 300
Db 241 FTTGSDDATCRLFLRADQELTAYSHESITGITSVAFLSGRLFAGYDDFNCNVWDSL 300
QY 301 KCERAGVLSGHDNRVSCLGVTADGMAVATGWSWDFLKIWN 340
Db 301 KGRAGVLAGHDNRVSCLGVTADGMAVATGWSWDFLKIWN 340

```

RESULT 7

T20830

hypothetical protein F13D12.7 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T20830
 R:Coles, L.

submitted to the EMBL Data Library, April 1995
 A:Reference number: Z19330
 A:Accession: T20830

A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-340 <WIL>
 A:Cross-references: EMBL:Z49127; PIDN:CAA88948.1; GSPDB:GN00020; CESP:F13D12.7
 A:Experimental source: clone F13D12
 C:Genetics:

A:Gene: CESP:F13D12.7
 A:Map position: 2
 A:Introns: 19/3; 57/3; 89/3; 116/1; 166/2; 209/3; 233/3; 306/1
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

Query Match
 Best local Similarity 84.0%; Score 1520; DB 2; Length 340;
 Matches 276; Conservative 31; Mismatches 33; Indels 0; Gaps 0;

```

QY 1 MGEMQLKQEAQKQIADARACADITLAEVLGVEVGRVQMRTRRLRGLAKIYA 60
Db 1 MSELQDLKQEAQKQIADARACADITLAEVLGVEVGRVQMRTRRLRGLAKIYA 60
QY 61 MHMATDSKLLVASASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
Db 61 MHMTDSRLLVASASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSIYSLKSRGNVKSRELKSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQOKTVE 180
Db 121 CSIYSLKTRGNVKSRELKSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQOKTVE 180
QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
Db 181 AGHSGDVMSLSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
QY 241 ICTGSDDASCRLFLRADQELTAYSHESITGITSVAFLSGRLFAGYDDFNCNVWDSL 300
Db 241 FTTGSDDATCRLFLRADQELTAYSHESITGITSVAFLSGRLFAGYDDFNCNVWDSL 300
QY 301 KCERAGVLSGHDNRVSCLGVTADGMAVATGWSWDFLKIWN 340
Db 301 KGRAGVLAGHDNRVSCLGVTADGMAVATGWSWDFLKIWN 340

```

```

Db 301 RQERAGVLAGHDNRVSCLGVTEDGMAVCTGWSWDFLKIWN 340

```

RESULT 8

RQKWB

GTP-binding regulatory protein beta chain - *Caenorhabditis elegans*
 N:Alternate names: guanine nucleotide binding protein beta chain; heterotrimeric G-protein
 C:Species: *Caenorhabditis elegans*
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: S09591

R:van der Voorn, L.; Gebbink, M.; Plasterk, R.H.A.; Ploegh, H.L.

J. Mol. Biol. 213, 17-26, 1990

A:Title: Characterization of a G-protein beta-subunit gene from the nematode *Caenorhabditis elegans*

A:Reference number: S09591; MUID:90250769

A:Accession: S09591

A:Molecule type: DNA

A:Residues: 1-340 <VAN>

A:Cross-references: EMBL:X17497; NID:g6642; PIDN:CAA35532.1; PID:g6643

C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that regulate the beta and gamma chains, required for GTPase activity, appear to be common to

C:Comment: In mammals, four distinct types of beta chains have been found.

C:Genetics:

A:Introns: 19/3; 57/3; 89/3; 115/2; 166/1; 209/3; 233/3; 305/2

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C:Keywords: GTP binding; heterotrimer; signal transduction

F:51-84/Domain: WD repeat homology <WD1>

F:88-126/Domain: WD repeat homology <WD2>

F:139-171/Domain: WD repeat homology <WD3>

F:180-213/Domain: WD repeat homology <WD4>

F:222-255/Domain: WD repeat homology <WD5>

F:263-299/Domain: WD repeat homology <WD6>

F:308-340/Domain: WD repeat homology <WD7>

Query Match
 Best local Similarity 83.7%; Score 1515; DB 1; Length 340;
 Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

```

QY 1 MGEMQLKQEAQKQIADARACADITLAEVLGVEVGRVQMRTRRLRGLAKIYA 60
Db 1 MSELQDLKQEAQKQIADARACADITLAEVLGVEVGRVQMRTRRLRGLAKIYA 60
QY 61 MHMATDSKLLVASASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
Db 61 MHMTDSRLLVASASQDGKLIWDTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSIYSLKSRGNVKSRELKSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQOKTVE 180
Db 121 CSIYSLKTRGNVKSRELKSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQOKTVE 180
QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
Db 181 AGHSGDVMSLSPDYKLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
QY 241 ICTGSDDASCRLFLRADQELTAYSHESITGITSVAFLSGRLFAGYDDFNCNVWDSL 300
Db 241 FTTGSDDATCRLFLRADQELTAYSHESITGITSVAFLSGRLFAGYDDFNCNVWDSL 300
QY 301 KCERAGVLSGHDNRVSCLGVTADGMAVATGWSWDFLKIWN 340
Db 301 KGRAGVLAGHDNRVSCLGVTEDGMAVCTGWSWDFLKIWN 340

```

RESULT 9

RGMSB4

GTP-binding regulatory protein beta-4 chain - mouse

N:Alternate names: guanine nucleotide binding protein beta-4 chain; heterotrimeric G-protein

C:Species: *Mus musculus* (house mouse)

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C:Accession: J50669

R: von Weizsäcker, E.; Strathmann, M.P.; Simon, M.I.

Biochem. Biophys. Res. Commun. 183, 350-356, 1992

A:Title: Diversity among the beta subunits of heterotrimeric GTP-binding proteins: chara
A:Reference number: JS0669; MUID:92181467
A:Accession: JS0669

A:Molecule type: mRNA
A:Residues: 1-340 <VON>

A:Cross-references: GB:S66124; NID:g246469; PIDN:AAB21609.1; PID:g246470
C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
ains. The beta and gamma chains, required for GTPase activity, appear to be common to all
rase; it is specific for each type of G protein.

C:Comment: In mammals, four distinct types of beta chains have been found.
C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C:Keywords: GTP binding; heterotrimer; signal transduction

F:51-84/Domain: WD repeat homology <WD1>
F:88-126/Domain: WD repeat homology <WD2>
F:139-171/Domain: WD repeat homology <WD3>
F:180-213/Domain: WD repeat homology <WD4>
F:222-255/Domain: WD repeat homology <WD5>
F:263-299/Domain: WD repeat homology <WD6>
F:308-340/Domain: WD repeat homology <WD7>

Query Match 82.5%; Score 1493; DB 1; Length 340;
Best Local Similarity 79.1%; Pred. No. 3.3e-116;
Matches 269; Conservative 37; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGEMEQLEAEQKQIADARKACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYA 60
1 MSELQLEAEQKQIADARKACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYA 60
Db 1 MHWATDSKLVASASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
61 MHWATDSKLVASASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
Db 61 MHWGYSRLVYASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSISLSKREGNVKVSRELTAHTGYLSCRFLLDNNIVTSSGDTTCALWDIETGQKTVF 180
121 CSISLSKREGNVKVSRELTAHTGYLSCRFLLDNNIVTSSGDTTCALWDIETGQKTVF 180
Db 121 CSISLSKREGNVKVSRELTAHTGYLSCRFLLDNNIVTSSGDTTCALWDIETGQKTVF 180
QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
Db 181 TGHSGDVMSLSPDLKTFVSGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
QY 241 ICTGSDASCRFLDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 300
241 ICTGSDASCRFLDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 300
Db 241 FATGSDATCRFLDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 300
QY 301 KCEYGVLSGHDNRVSCIGVTADGMVATGSMDFLKIWN 340
301 KCEYGVLSGHDNRVSCIGVTADGMVATGSMDFLKIWN 340
Db 301 KGRSGVLGHGHDNRVSCIGVTADGMVATGSMDFLKIWN 340

RESULT 10
S34348
GTP-binding regulatory protein beta chain - great pond snail

N:Alternate names: guanine nucleotide binding protein beta chain

C:Species: Lymnaea stagnalis (great pond snail)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999

C:Accession: S69891; S34348

R:Knoll, J.C.; Roovers, E.; van Kesteren, E.R.; Planta, R.J.; Vreugdenhil, E.; van Heerik

Biochim. Biophys. Acta 1222, 129-133, 1994

A:Title: A G-protein beta subunit that is expressed in the central nervous system of the

A:Reference number: S69891; MUID:94242793

A:Accession: S69891

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-341 <KN2>

A:Cross-references: EMBL:Z23105; NID:g312631; PIDN:CAA80652.1; PID:g312632

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

F:52-85/Domain: WD repeat homology <WD1>

F:181-214/Domain: WD repeat homology <WD4>

F:267-300/Domain: WD repeat homology <WD6>

F:309-341/Domain: WD repeat homology #status atypical <WD7>

Query Match 81.9%; Score 1482; DB 2; Length 341;
Best Local Similarity 80.2%; Pred. No. 2.7e-115;
Matches 271; Conservative 29; Mismatches 38; Indels 0; Gaps 0;

QY 3 EMEQLEAEQKQIADARKACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYAMH 62
3 EMEQLEAEQKQIADARKACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYAMH 62
Db 4 DLEALRQETEDQKQIADARKACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYAMH 63
QY 63 WATDSKLVASASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 122
63 WATDSKLVASASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 122
Db 64 WATDSKLVASASQDGLIWDYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 123
QY 123 IYSLKREGNVKVSRELTAHTGYLSCRFLLDNNIVTSSGDTTCALWDIETGQKTVFV 182
123 IYSLKREGNVKVSRELTAHTGYLSCRFLLDNNIVTSSGDTTCALWDIETGQKTVFV 182
Db 124 IYSLKREGNVKVSRELTAHTGYLSCRFLLDNNIVTSSGDTTCALWDIETGQKTVFV 183
QY 183 HTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 242
183 HTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 242
Db 184 HTGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 243
QY 243 TGSDDASCRFLDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 302
243 TGSDDASCRFLDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 302
Db 244 TGSDDATCRFLDLRADQELTAYSHESITGITSVAFLSGRLIFAGYDDFNCNVWDSL 303
QY 303 ERVGVLSGHDNRVSCIGVTADGMVATGSMDFLKIWN 340
303 ERVGVLSGHDNRVSCIGVTADGMVATGSMDFLKIWN 340
Db 304 ETHGVLAGHDNRVSCIGVTADGMVATGSMDFLKIWN 341

RESULT 11

RGROB2
GTP-binding regulatory protein beta-2 chain - bovine (fragment)

N:Alternate names: guanine nucleotide binding protein beta-2 chain; heterotrimeric G-

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C:Accession: A26617; A28040

R:Fong, H.K.W.; Amatruda III, T.T.; Birren, B.W.; Simon, M.I.

Proc. Natl. Acad. Sci. U.S.A. 84, 3792-3796, 1987

A:Title: Distinct forms of the beta-subunit of GTP-binding regulatory proteins identi

A:Reference number: A94155; MUID:87231903

A:Accession: A26617

A:Molecule type: mRNA

A:Residues: 1-326 <RON>

A:Cross-references: GB:M16539; NID:g163112; PIDN:AAA30553.1; PID:g163113

R:Gao, B.; Gilman, A.G.; Robishaw, J.D.

Proc. Natl. Acad. Sci. U.S.A. 84, 6122-6125, 1987

A:Title: A second form of the beta subunit of signal-transducing G proteins.

A:Reference number: A94177; MUID:87317607

A:Accession: A28040

A:Molecule type: mRNA

A:Residues: 88-270, 272-302 <GAO>

A:Cross-references: GB:M16539; NID:g163110; PIDN:AAA30552.1; PID:g163111

C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re

ains. The beta and gamma chains, required for GTPase activity, appear to be common to

rase; it is specific for each type of G protein.

C:Comment: In mammals, four distinct types of beta chains have been found.

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C:Keywords: GTP binding; heterotrimer; signal transduction

F:37-70/Domain: WD repeat homology <WD1>

F:74-112/Domain: WD repeat homology <WD2>

F:125-157/Domain: WD repeat homology <WD3>

F:166-199/Domain: WD repeat homology <WD4>

F:208-241/Domain: WD repeat homology <WD5>

F:249-285/Domain: WD repeat homology <WD6>

F:294-326/Domain: WD repeat homology <WD7>

Query Match 81.1%; Score 1467; DB 1; Length 326;
Best Local Similarity 81.0%; Pred. No. 4.5e-114;
Matches 264; Conservative 29; Mismatches 33; Indels 0; Gaps 0;

QY 15 KQIADARKACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYAMWATDSKLVAS 74
15 KQIADARKACADITLAEVSGLEVGRVQMRTRTLRGHLAKIYAMWATDSKLVAS 74

Db 1 RNQIRDAKACGSDSTLTQITAGLDVPVGRIOQRTIRTLRGLAKIYAMHMGCTDSRLVSAS 60
 QY 75 QDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNEFVACGGLDNMCSTYSLKSRGNV 134
 Db 61 QDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNEFVACGGLDNMCSTYSLKSRGNV 120
 QY 135 VSRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGOQKTFVGHGTGDCMSLAVSP 194
 Db 121 VSRELPHGTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGOQKTFVGHGTGDCMSLAVSP 180
 QY 195 DYKLFISGACDASAKIMDVREGTCRQTFGTGHSIDINAICTFPNGEAICTGSDASCRLFD 254
 Db 181 DGRTEVSGACDASAKIMDVREGTCRQTFGTGHSIDINAVAFPPNGYAFTTGSDDATCRLFD 240
 QY 255 LRADQELTAYSHESIIGITSVAFSLSGRLFAGYDDFNCNWDLSKCEKERVGLSGHDNR 314
 Db 241 LRADQELTAYSHESIIGITSVAFSLSGRLFAGYDDFNCNWDLSKCEKERVGLSGHDNR 300
 QY 315 VSCLGVTADGMAVATGSDSFLKIWN 340
 Db 301 VSCLGVTADGMAVATGSDSFLKIWN 326

RESULT 12

RGOFBE

GTP-binding regulatory protein beta chain - northern European squid

N:Alternate names: guanine nucleotide binding protein beta chain; heterotrimeric G-protein; Loligo forbesi (northern European squid)

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

R:Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Findlay, J.B.C.

A:Title: Sequence of the beta-subunit of the phosphatidylinositol-specific phospholipase A:Reference number: S13302; MUID:91113146

A:Accession: S13302

A:Molecule type: mRNA

A:Residues: 1-341 <RYB>

A:Cross-references: EMBL:X56757; NID:g9507; PIDN:CAA40077.1; PID:g9508

C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C:Keywords: GTP binding; heterotrimer; signal transduction

F:52-85/Domain: WD repeat homology <WD1>

F:89-127/Domain: WD repeat homology <WD2>

F:140-172/Domain: WD repeat homology <WD3>

F:181-214/Domain: WD repeat homology <WD4>

F:223-256/Domain: WD repeat homology <WD5>

F:264-300/Domain: WD repeat homology <WD6>

F:309-341/Domain: WD repeat homology <WD7>

Query Match 81.1%; Score 1467; DB 1; Length 341;

Best Local Similarity 79.9%; Pred. No. 4.8e-114;

Matches 270; Conservative 30; Mismatches 38; Indels 0; Gaps 0;

QY 3 EMEQLKQEAQOLKQIADAKACADITLAEVSGLEVGRVQMTTRTLRGLAKIYAMH 62
 Db 4 ELEALRQETEQKQIARAKAADITLAMATANEPVGRQMTTRTLRGLAKIYAMH 63
 QY 63 WATDSKLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNEFVACGGLDNMC 122
 Db 64 WASDSRLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNEFVACGGLDNMC 123
 QY 123 IYSLKSRGNVSVRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGOQKTFV 182
 Db 124 IYSLKTRGNVSVRELPHGTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGOQKTFV 183
 QY 183 HTGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQTFGTGHSIDINAICTFPNGEA 242
 Db 184 HTGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQTFGTGHSIDINAICTFPNGEA 243
 QY 243 TGSDDASCRFLDLRADQELTAYSHESIIGITSVAFSLSGRLFAGYDDFNCNWDLSKC 302

Db 244 TGSDDATCRLFDLRADQELTAYSHESIIGITSVAFSLSGRLFAGYDDFNCNWDLSKC 303
 QY 303 ERVGLSGHDNRVSCGLVTADGMAVATGSDSFLKIWN 340
 Db 304 ERAGVLGHGHDNRVSCGLVTEDGMAVATGSDSFLKIWN 341

RESULT 13

RGFFBH

GTP-binding regulatory protein beta chain homolog - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

R:Yarfitz, S.; Provost, N.M.; Hurley, J.B.

Proc. Natl. Acad. Sci. U.S.A. 85, 7134-7138, 1988

A:Title: Cloning of a Drosophila melanogaster guanine nucleotide regulatory protein b

A:Reference number: A40489; MUID:89017152

A:Accession: A40489

A:Molecule type: mRNA

A:Residues: 1-340 <YAR>

A:Cross-references: GB:M22567; GB:J04083; NID:g157497; PIDN:AAB59247.1; PID:g157498

A:Genetics:

A:Gene: FlyBase:Gabyr

A:Cross-references: FlyBase:FBgn0001105

A:Map position: X13F

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

F:51-84/Domain: WD repeat homology <WD1>

F:88-126/Domain: WD repeat homology <WD2>

F:139-171/Domain: WD repeat homology <WD3>

F:180-213/Domain: WD repeat homology <WD4>

F:222-255/Domain: WD repeat homology <WD5>

F:263-299/Domain: WD repeat homology <WD6>

F:308-340/Domain: WD repeat homology <WD7>

Query Match 80.3%; Score 1452; DB 1; Length 340;

Best Local Similarity 76.5%; Pred. No. 8.3e-113;

Matches 260; Conservative 38; Mismatches 42; Indels 0; Gaps 0;

QY 1 MGEMQLKQEAQOLKQIADAKACADITLAEVSGLEVGRVQMTTRTLRGLAKIYAMH 60
 Db 1 MNELDLRQEAQOLKQIADAKACADITLAEVSGLEVGRVQMTTRTLRGLAKIYAMH 60
 QY 61 MHWATDSKLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNEFVACGGLDNMC 120
 Db 61 MHWGNDSRLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAVAPSGNEFVACGGLDNMC 120
 QY 121 CSIYSLKSRGNVSVRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGOQKTF 180
 Db 121 CSIYNLKTREGNVSRELPHGTGYLSCCRFLDDNNIVTSSGDMSCGLWDIETGLQVTSF 180
 QY 181 VGHGTGDCMSLAVSPDYKLFISGACDASAKIMDVREGTCRQTFGTGHSIDINAICTFPNGEA 240
 Db 181 LGHTGDVWALSLAPDQCKTFVSGACDASAKIMDVREGTCRQTFGTGHSIDINAICTFPNGEA 240
 QY 241 ICTGSDASCRFLDLRADQELTAYSHESIIGITSVAFSLSGRLFAGYDDFNCNWDLS 300
 Db 241 FATGSDATCRLFDLRADQELTAYSHESIIGITSVAFSLSGRLFAGYDDFNCNWDLS 300
 QY 301 KCERGVLSGHGHDNRVSCGLVTADGMAVATGSDSFLKIWN 340
 Db 301 KAERSGILAGHDNRVSCGLVTENGMAVATGSDSFLKIWN 340

RESULT 14

A47370

GTP-binding regulatory protein beta chain - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum

C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999

R:Lilly, P.; Wu, L.; Welker, D.L.; Devreotes, P.N.

Genes Dev. 7, 986-995, 1993

A;Title: A G-protein beta-subunit is essential for Dictyostelium development.
A;Reference number: A47370; MUID:93279474
A;Accession: A47370
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-347 <LIL>
A;Cross-references: GB:X73641; NID:g460980; PIDN:CAA52018.1; PID:g460981
A;Note: sequence extracted from NCBI backbone (NCBIN:132987, NCBIN:132989, NCBIN:132991,
C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
F;146-178/Domain: WD repeat homology <WD2>
F;187-220/Domain: WD repeat homology <WD3>
F;273-306/Domain: WD repeat homology <WD5>
F;315-347/Domain: WD repeat homology #status atypical <WD6>

Query Match 67.7%; Score 1225; DB 2; Length 347;
Best Local Similarity 66.4%; Pred. No. 5.5e-94;
Matches 225; Conservative 46; Mismatches 66; Indels 2; Gaps 1;

QY 3 EMEQLKQAEOLKQIADARKACADITLAEVLVSGLEVGRVQ--MRTRTLRLGHLAKIYA 60
Db 8 KIQOARRDAESMKEQIRANRDVYNDTTLKFTTRDLPGLPKMEGKIKVRRNLKGLAKIYA 67
QY 61 MHWATDSKLLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAAYAPSGNEFVACGGLDNM 120
Db 68 MHWAEEDNVHLVSASQDGKLIWDTLTNKVHAIPLRSSWMTCAAYSPANFVACGGLDNI 127
QY 121 CSITSLKSRGNVKSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQKTYF 180
Db 128 CSITNLSRREQPIRVCRELNHTGYLSCCRFLNDRQIVTSSGDMTCILWDVENGTKITEF 187
QY 181 VGHGDCMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
Db 188 SDHNGDVMSVSPDKNYFISGACDATALMDLRSGRCVQFTGHEDINAVQYFPNGLS 247
QY 241 ICTGSDDASCRLFLRADQELTAYSHESIICGITSVAFSLSGRLLFAGYDDFNCNWD 300
Db 248 FGTGSDDASCRLFLRADRELMQYTHDNILCGITSVGFSGRFLFAGYDDFTCNWDTL 307
QY 301 KCEKRVGLSGHDNRVSCLGVTADGMAVATGSWDSFLKIW 339
Db 308 KGERVLSLTGHGNRVSCLGVTADGMACTGSWDSFLKIW 346

RESULT 15
A54969
beta-5 GTP-binding protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 13-Aug-1999
C;Accession: A54969
R;Watson, A.J.; Katz, A.; Simon, M.I.
J. Biol. Chem. 269, 22150-22156, 1994
A;Title: A fifth member of the mammalian G-protein beta-subunit family. Expression in br
A;Reference number: A54969; MUID:94350964
A;Accession: A54969
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-353 <WAT>
A;Cross-references: GB:L34290; NID:g1237255; PIDN:AAA93084.1; PID:g557738
C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
F;59-92/Domain: WD repeat homology <WD1>
F;149-182/Domain: WD repeat homology <WD3>
F;193-226/Domain: WD repeat homology <WD4>
F;279-312/Domain: WD repeat homology <WD6>
F;321-353/Domain: WD repeat homology #status atypical <WD7>

Query Match 52.3%; Score 945.5; DB 2; Length 353;
Best Local Similarity 51.6%; Pred. No. 8e-71;
Matches 176; Conservative 57; Mismatches 103; Indels 5; Gaps 3;

QY 4 MEQLKQAEOLKQIADARKACADITLAEVLVSGLEVGRVQMRTRRTLRLGHLAKIYAMHW 63
: || || || || : : | : | : : : | : || || || || | : | |

Db 12 LASLKSEAEISLKGKLEERAKLHVDVHQAERVEALGQFVMTKTRRTLKGHNKYLQMDW 71
QY 64 ATDSKLLVSASQDGKLIWDTYTTNKVHAIPLRSSWMTCAAYAPSGNEFVACGGLDNMCSI 123
Db 72 CKDKRRIVSSQDGKVIWDSFTTNKEHAVTMCPTWVMACAYAPSGCAIACGGLDNKCSV 131
QY 124 YSL--KSREGNVKVSRELSAHTGYLSCCRFLD--DNNIVTSSGDTTCALWDIETGQKTYF 180
Db 132 YPLTFDKNENNAKKKSVAMHTNYLSACSFNSDMQILTASGDTTCALWDVESGQLQSF 191
QY 181 VGHGTD--CMSLAVSPDYKLFISGACDASAKLMDVREGTCRQFTGHESDINAICFPNG 238
Db 192 HGHGADVLCILDAPSETGNTFVSGGCDKKAMVWDMRSGQCVAFETHESDVNSVRYTPSG 251
QY 239 EAICTGSDDASCRLFLRADQELTAYSHESIICGITSVAFSLSGRLLFAGYDDFNCNWD 298
Db 252 DAFASGSDATCRLYDLRADREVAIYSKESIIFGASSVDFSLSGRLLFAGYNDYTNWWD 311
QY 299 SLKCEKRVGLSGHDNRVSCLGVTADGMAVATGSWDSFLKIW 339
Db 312 VLKGSRVSLTGHENRVSTLRVSPDGTAFCSGSWDHTLRVW 352

Search completed: September 28, 2001, 10:33:20
Job time: 271 sec

0
.
1

XX This sequence represents the human G-protein beta 3 subunit. A variant
 CC of the gene encoding this protein has applications in the diagnosis of
 CC diseases or assessing the risk of a disease associated with G-protein
 CC misregulation. G-protein misregulation is associated with G-protein
 CC cardiovascular diseases e.g. coronary heart disease, hypertension,
 CC stenosis, stroke and thrombosis, metabolic disorders such as diabetes,
 CC diabetic complications, disorders of lipid metabolism and central
 CC chemoreception dysfunction (e.g. sudden infant death syndrome), and
 CC immunological disorders such as impaired wound healing, tumours, AIDS,
 CC cirrhosis and transplant rejection.
 CC
 SQ Sequence 340 AA;

Query Match 100.0%; Score 1809; DB 19; Length 340;
 Best Local Similarity 100.0%; Pred. No. 5.3e-171;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMEDLRQEAQKQIADARKACADVTLLAEVLSGLEVGRVQMTTRRLRGHLAKIYA 60
 Db 1 mgemeqlrgeaqkqjadarkacadvllaelsvsglevgrvmtrtrtlrghlakiya 60
 QY 61 MHMATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWVMTCAVAPSGNFVACGGGLDNM 120
 Db 61 mhmatdskllvsasqdgkcliwdsyttknvhaiplrsswmtcayapsnfvacggldnm 120
 QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQKTVF 180
 Db 121 cslynlskregnvkvsrelsahgtysccrflddnnivtssgdttcaldietgqktvf 180
 QY 181 VGHGTGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCRQTFGTGHESDINAICFFPNGEA 240
 Db 181 vghtgdcmslavspdfnlfisgacdasaklmdvregtcrgtftghesdinaicffpgea 240
 QY 241 ICTGSDDASCRLFDLRADQELICFSHESIICGITSVAFLSGRLFFAGYDDFNCNVWDSM 300
 Db 241 ictgsddascrlfdlradqelicfshesiiicgitsvafslsgrllfagyddfncnvwdsm 300
 QY 301 KSERVGIISGHDNRVSCIGVTADGMAVATGSMDSFLKIWN 340
 Db 301 kservgilsghdnrvscigvtadgmavatsgswdsflkiwn 340

RESULT 2
 AAB15169
 ID AAB15169 standard; Protein; 340 AA.
 AC AAB15169;
 XX
 DT 12-DEC-2000 (first entry)
 DE Human Taste Cell specific G-protein beta 3 subunit.
 XX
 KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry.
 XX
 OS Homo sapiens.
 XX
 PN WO200045179-A2.
 XX
 PD 03-AUG-2000.
 XX
 PF 26-JAN-2000; 2000WO-US02218.
 XX
 PR 27-JAN-1999; 99US-0117404.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Zuker CS, Adler JE, Lindemeier J;
 XX
 DR WPI; 2000-49361/44.
 DR N-PSDB; AAA74591.

XX Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -
 XX
 PS Claim 1; Page 63; 68pp; English.
 XX

CC The present sequence is human G-protein beta 3 subunit. G-protein beta 3
 CC is expressed specifically in taste cells, hence this sequence is referred
 CC to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3
 CC is involved in the taste transduction pathway. TC-Gbeta3 may be used for
 CC identifying taste modulating compounds which can be used in
 CC pharmaceutical and food industries to customise taste.
 CC
 SQ Sequence 340 AA;

Query Match 100.0%; Score 1809; DB 21; Length 340;
 Best Local Similarity 100.0%; Pred. No. 5.3e-171;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMEDLRQEAQKQIADARKACADVTLLAEVLSGLEVGRVQMTTRRLRGHLAKIYA 60
 Db 1 mgemeqlrgeaqkqjadarkacadvllaelsvsglevgrvmtrtrtlrghlakiya 60
 QY 61 MHMATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWVMTCAVAPSGNFVACGGGLDNM 120
 Db 61 mhmatdskllvsasqdgkcliwdsyttknvhaiplrsswmtcayapsnfvacggldnm 120
 QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQKTVF 180
 Db 121 cslynlskregnvkvsrelsahgtysccrflddnnivtssgdttcaldietgqktvf 180
 QY 181 VGHGTGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCRQTFGTGHESDINAICFFPNGEA 240
 Db 181 vghtgdcmslavspdfnlfisgacdasaklmdvregtcrgtftghesdinaicffpgea 240
 QY 241 ICTGSDDASCRLFDLRADQELICFSHESIICGITSVAFLSGRLFFAGYDDFNCNVWDSM 300
 Db 241 ictgsddascrlfdlradqelicfshesiiicgitsvafslsgrllfagyddfncnvwdsm 300
 QY 301 KSERVGIISGHDNRVSCIGVTADGMAVATGSMDSFLKIWN 340
 Db 301 kservgilsghdnrvscigvtadgmavatsgswdsflkiwn 340

RESULT 3
 AAY67865
 ID AAY67865 standard; protein; 340 AA.
 AC AAY67865;
 XX
 DT 25-APR-2000 (first entry)
 DE Human Hgb3 G-protein beta3 subunit amino acid sequence.
 XX
 KW Ste20p/PAK; G-protein-coupled receptor signal transduction; human; Hgb3;
 KW Ste4p/Gbeta interaction domain; p21-activated protein kinase;
 KW G-protein coupled receptor signal transduction;
 XX
 OS Homo sapiens.
 XX
 PN CA2219958-A1.
 XX
 PD 07-JUL-1999.
 XX
 PF 07-JAN-1998; 98CA-2219958.
 XX
 PR 07-JAN-1998; 98CA-2219958.
 XX
 PA (LEBE/) LEBERER E.
 PA (LEEU/) LEEUW T.

PA (THOM/) THOMAS D Y.
XX (WHIT/) WHITEMAY M.
PI Leberer E, Leeuw T, Thomas DY, Whiteway M;
XX WPI: 2000-137553/13.

DR Interacting polypeptides involved in G-protein-coupled receptor signal
XX transduction -
PT
PS Claim 3; Fig 6; 91pp; English.

XX This sequence represents the beta3 subunit of a human G-protein. The
CC invention relates to the G-protein beta subunit interaction domain of the
CC Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein
CC kinases are p21-activated protein kinases (PAK), and they are involved in
CC many varied cellular processes ranging from morphogenesis and stress
CC response, to apoptosis. Interacting polypeptides Ste4p/Gbeta and
CC Ste20p/PAK are useful for designing in vitro and in vivo experimental
CC models which enable the screening of large collections of synthetic,
CC semi-synthetic, or natural compounds for therapeutic use in Ste4p/Gbeta
CC and Ste20p/PAK dependent diseases.

XX Sequence 340 AA;

Query Match 100.0%; Score 1809; DB 21; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.3e-171;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGEMEQLRQAEOLKKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
Db 1 mgemeqlrqaeeqlkkqiadarkacadvlaelvsylevgrvmtrrlrghlakiya 60
OY 61 MHWATDSKLVASASQDGLIWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
Db 61 mhwatdsklvvasasqdgkllwdsytltnkvhaiplrswmtcayapsnfvacgglndm 120
OY 121 CSIYNLKSREGNVKVSRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQKTVF 180
Db 121 csiynlksregnvkvsrelsahthgylsccrflddnnivtssgdtcalwdietgqktvf 180
OY 181 VGHGTDCMSLAVSPDFNLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
Db 181 vghtgdcmslavspdfnlfisgacdasaklmdvregtcroftghesdinaicfipngea 240
OY 241 ICTGSDASCRFLDLRADQELICFSHESIICGITSVAFLSGRLFAGYDDFNCNWDMSM 300
Db 241 ictgsddascrlfldlradoelicfshesiiicgitsvafslsgrlffagyddfncnwdmsm 300
OY 301 KSERVGIILSGHDNRVSCLGVTADGMAVATGSWDSFLKIWN 340
Db 301 kservgilsghdnrvsclgvtadgmavatswdsfkiwn 340

RESULT 4
AAB15173
ID AAB15173 standard; Protein; 340 AA.
XX
XX AAB15173;
AC
XX 12-DEC-2000 (first entry)
DT
XX
XX Mutant human Taste Cell specific G-protein beta 3 subunit variant #1.
DE
XX
XX Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
KW taste transduction pathway; pharmaceutical; food industry; mutation;
KW mutant; mutant.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers

FT Misc-difference 7 /note= "wild-type leu substituted by ile"
FT
XX
XX PN WO200045179-A2.
XX
XX PD 03-AUG-2000.
XX
XX PF 26-JAN-2000; 2000WO-US02218.
XX
XX PR 27-JAN-1999; 99US-0117404.
XX
XX PA (REGC) UNIV CALIFORNIA.
XX
XX PI Zuker CS, Adler JE, Lindemeier J;
XX
XX DR WPI: 2000-499361/44.

XX Identifying a compound that modulates sensory signaling in sensory
PT cells for use in pharmaceutical and food industries comprises
PT contacting the compound with a sensory cell specific G-protein beta
PT polypeptide -
PS
XX Disclosure; Page -; 68pp; English.

XX The present sequence is a mutant human G-protein beta 3 subunit.
CC G-protein beta 3 is expressed specifically in taste cells, hence this
CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
CC TC-Gbeta3 may be used for identifying taste modulating compounds which
CC can be used in pharmaceutical and food industries to customise taste.
CC Note: The present sequence is not shown in the specification but is
CC derived from the human wild-type TC-Gbeta3 sequence given on page 63
CC (see AAB15169) and information given on page 8 of the disclosure.

XX Sequence 340 AA;

Query Match 99.9%; Score 1807; DB 21; Length 340;
Best Local Similarity 99.7%; Pred. No. 8.4e-171;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGEMEQLRQAEOLKKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
Db 1 mgemeqlrqaeeqlkkqiadarkacadvlaelvsylevgrvmtrrlrghlakiya 60
OY 61 MHWATDSKLVASASQDGLIWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
Db 61 mhwatdsklvvasasqdgkllwdsytltnkvhaiplrswmtcayapsnfvacgglndm 120
OY 121 CSIYNLKSREGNVKVSRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQKTVF 180
Db 121 csiynlksregnvkvsrelsahthgylsccrflddnnivtssgdtcalwdietgqktvf 180
OY 181 VGHGTDCMSLAVSPDFNLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
Db 181 vghtgdcmslavspdfnlfisgacdasaklmdvregtcroftghesdinaicfipngea 240
OY 241 ICTGSDASCRFLDLRADQELICFSHESIICGITSVAFLSGRLFAGYDDFNCNWDMSM 300
Db 241 ictgsddascrlfldlradoelicfshesiiicgitsvafslsgrlffagyddfncnwdmsm 300
OY 301 KSERVGIILSGHDNRVSCLGVTADGMAVATGSWDSFLKIWN 340
Db 301 kservgilsghdnrvsclgvtadgmavatswdsfkiwn 340

RESULT 5
AAB15174
ID AAB15174 standard; Protein; 340 AA.
XX
XX AAB15174;
AC
XX 12-DEC-2000 (first entry)
DT

XX DE Mutant human Taste Cell specific G-protein beta 3 subunit variant #2.
 XX KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 KW mutant; mutant.
 XX OS Homo sapiens.
 OS Synthetic.

XX Key
 XX Location/Qualifiers
 XX Misc-difference 161
 XX /note= "Wild-type Ser substituted by Thr"

PN WO200045179-A2.
 XX 03-AUG-2000.
 PD 26-JAN-2000; 2000WO-US02218.
 PF 27-JAN-1999; 99US-0117404.
 PR (REGC) UNIV CALIFORNIA.
 PA Zuker CS, Adler JE, Lindemeier J;
 PI WPI; 2000-499361/44.
 DR
 XX

PT Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -

PS Disclosure; Page -: 68pp; English.

CC The present sequence is a mutant human G-protein beta 3 subunit.
 CC G-protein beta 3 is expressed specifically in taste cells, hence this
 CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
 CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
 CC TC-Gbeta3 may be used for identifying taste modulating compounds which
 CC can be used in pharmaceutical and food industries to customise taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type TC-Gbeta3 sequence given on page 63
 CC (see AAB15169) and information given on page 8 of the disclosure.
 CC
 XX
 SQ Sequence 340 AA;

Query Match 99.8%; Score 1806; DB 21; Length 340;
 Best Local Similarity 99.7%; Pred. No. 1.1e-170;
 Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMEQLRQAEQOLKKQIADARKACADVTLAELVSGLEVGRVQMTTRTLRGHLAKIYA 60
 DB 1 mgemeqlrqaegqlkkqladarkacadvlaelvsqlevgrvqmttrtlrghlakiya 60
 QY 61 MHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAYPASGNEVACGGLDMM 120
 DB 61 mhwatdskllvsasqdgkcliwdsyttknvhaiplrsswmtcayapsgnevacgglidmm 120
 QY 121 CSIYNLKSREGNVKVSRELSAHGTGLSCRFLLDDNNIVTSSGDTTCALMDIETGOQKTVF 180
 DB 121 csiynlksregnvkvsrelsahgtglscrfllddnnivtssgdttcaldietgqktvf 180
 QY 181 VGHGTGDCMSLAVSPDFNLFIGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
 DB 181 vghtgdcmslavspdfnlfigacdasaaklmdvregtcroftghesdinaiicfpngea 240
 QY 241 ICTGSDASCRFLDLRADDELICFSHESIICITVSVAFLSGRLLFAGYDDFNCNVWDSM 300
 DB 241 ictgsddascrifldraddelicfshesiiicitvsafslsgrllfagyddfncnvwds 300
 QY 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGWSWDSFLKIWN 340

DB 301 kservglsghndnrsvclgvtadgmaavatgswdsflkiwn 340

RESULT 6
 AAB15175
 ID AAB15175 standard; Protein; 340 AA.
 XX
 AC AAB15175;
 DT 12-DEC-2000 (first entry)
 XX

DE Mutant human Taste Cell specific G-protein beta 3 subunit variant #3.
 KW Human; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
 KW taste transduction pathway; pharmaceutical; food industry; mutation;
 KW mutant; mutant.
 XX OS Homo sapiens.
 OS Synthetic.

XX Key
 XX Location/Qualifiers
 XX Misc-difference 301
 XX /note= "Wild-type Lys substituted by Arg"

PN WO200045179-A2.
 XX 03-AUG-2000.
 PD 26-JAN-2000; 2000WO-US02218.
 PF 27-JAN-1999; 99US-0117404.
 PR (REGC) UNIV CALIFORNIA.
 PA Zuker CS, Adler JE, Lindemeier J;
 PI WPI; 2000-499361/44.
 DR
 XX

PT Identifying a compound that modulates sensory signaling in sensory
 PT cells for use in pharmaceutical and food industries comprises
 PT contacting the compound with a sensory cell specific G-protein beta
 PT polypeptide -

PS Disclosure; Page -: 68pp; English.

CC The present sequence is a mutant human G-protein beta 3 subunit.
 CC G-protein beta 3 is expressed specifically in taste cells, hence this
 CC sequence is referred to as Taste Cell specific G-protein beta 3 subunit
 CC (TC-Gbeta3). TC-Gbeta3 is involved in the taste transduction pathway.
 CC TC-Gbeta3 may be used for identifying taste modulating compounds which
 CC can be used in pharmaceutical and food industries to customise taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type TC-Gbeta3 sequence given on page 63
 CC (see AAB15169) and information given on page 8 of the disclosure.
 CC
 XX
 SQ Sequence 340 AA;

Query Match 99.8%; Score 1806; DB 21; Length 340;
 Best Local Similarity 99.7%; Pred. No. 1.1e-170;
 Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMEQLRQAEQOLKKQIADARKACADVTLAELVSGLEVGRVQMTTRTLRGHLAKIYA 60
 DB 1 mgemeqlrqaegqlkkqladarkacadvlaelvsqlevgrvqmttrtlrghlakiya 60
 QY 61 MHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAYPASGNEVACGGLDMM 120
 DB 61 mhwatdskllvsasqdgkcliwdsyttknvhaiplrsswmtcayapsgnevacgglidmm 120
 QY 121 CSIYNLKSREGNVKVSRELSAHGTGLSCRFLLDDNNIVTSSGDTTCALMDIETGOQKTVF 180
 DB 121 csiynlksregnvkvsrelsahgtglscrfllddnnivtssgdttcaldietgqktvf 180

Db 121 cslynksregnvksrelsahtgylsccrflldnnivtssgdtlcalwdietgqktvf 180
QY 181 VGHGDCMSLAVSPDENLFTSGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
Db 181 vghtgdcmslavspdenlftsgacdasaklmdvregtcrcftghesdinaicfpngea 240
QY 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFSLSGRLLFAGYDDFNCNWDSM 300
Db 241 ictgsddascrlfdlraddgelicfshesicgitsvafslsgrllfagyddfncnwds 300
QY 301 KSERVGILSGHDNRVSCLGVTADGMVAATGSDSFLKIMN 340
Db 301 rservgilsghdnrsvclgvtadgmavatgswdsflkiwn 340

RESULT 7
AAB15170
ID AAB15170 standard; Protein; 340 AA.
XX
AC AAB15170;
XX
DT 12-DEC-2000 (first entry)
DE Mutant rat Taste Cell specific G-protein beta 3 subunit variant #1.
XX
KW Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
KW taste transduction pathway; pharmaceutical; food industry; mutation;
KW mutein; mutant.
XX
OS Rattus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 8 /note= "Wild-type Lys substituted by Arg"
FT
XX
PN WO200045179-A2.
XX
PD 03-AUG-2000.
XX
PF 26-JAN-2000; 2000WO-US02218.
XX
PR 27-JAN-1999; 99US-0117404.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Zuker CS, Adler JE, Lindemeier J;
XX
DR WPI; 2000-499361/44.
XX
PT Identifying a compound that modulates sensory signaling in sensory
PT cells for use in pharmaceutical and food industries comprises
PT contacting the compound with a sensory cell specific G-protein beta
PT polypeptide -
XX
PS Disclosure; Page -: 68pp; English.
XX
CC The present sequence is a mutant rat G-protein beta 3 subunit. G-protein
CC beta 3 is expressed specifically in taste cells, hence this sequence is
CC referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).
CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
CC be used for identifying taste modulating compounds which can be used in
CC pharmaceutical and food industries to customise taste.
CC Note: The present sequence is not shown in the specification but is
CC derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
CC AAB15168) and information given on page 8 of the disclosure.
XX
SQ Sequence 340 AA;

Query Match 97.6%; Score 1765; DB 21; Length 340;
Best Local Similarity 96.8%; Pred. No. 1.2e-166;
Matches 329; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAELKKQIADARKACADVTTLAEVLVSGLEVVGWQMRTRRTLRGHLAKTYA 60
Db 1 mgemeqlrqaeeqlkkqiadarkacadtllaelsvsglevvgwqmrtrrtlrghlakiya 60
QY 61 MHWATDSKLVASQDGKLIWDSYTTNKVHAIPLRSSWVMTCAYAPSGNFVACGGLDM 120
Db 61 mhwatdsklvassdqgkliwtdytltnkvhaiplrsswvmtcayapsnfvacggladm 120
QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQKTYV 180
Db 121 csylsksregnvksrelsahtgylsccrflldnnivtssgdtlcalwdietgqktvf 180
QY 181 VGHGDCMSLAVSPDENLFTSGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
Db 181 vghtgdcmslavspdklftsgacdasaklmdvregtcrcftghesdinaicfpngea 240
QY 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFSLSGRLLFAGYDDFNCNWDSM 300
Db 241 ictgsddascrlfdlraddgelitayshesicgitsvafslsgrllfagyddfncnwds 300
QY 301 KSERVGILSGHDNRVSCLGVTADGMVAATGSDSFLKIMN 340
Db 301 kservgilsghdnrsvclgvtadgmavatgswdsflkiwn 340

RESULT 8
AAB15168
ID AAB15168 standard; Protein; 340 AA.
XX
AC AAB15168;
XX
DT 12-DEC-2000 (first entry)
DE Rat Taste Cell specific G-protein beta 3 subunit.
XX
KW Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
KW taste transduction pathway; pharmaceutical; food industry.
XX
OS Rattus sp.
XX
PN WO200045179-A2.
XX
PD 03-AUG-2000.
XX
PF 26-JAN-2000; 2000WO-US02218.
XX
PR 27-JAN-1999; 99US-0117404.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Zuker CS, Adler JE, Lindemeier J;
XX
DR WPI; 2000-499361/44.
DR N-PSDB; AAA74590.
XX
PT Identifying a compound that modulates sensory signaling in sensory
PT cells for use in pharmaceutical and food industries comprises
PT contacting the compound with a sensory cell specific G-protein beta
PT polypeptide -
XX
PS Claim 1; Page 62; 68pp; English.
XX
CC The present sequence is rat G-protein beta 3 subunit. G-protein beta 3 is
CC expressed specifically in taste cells, hence this sequence is referred to
CC as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3). TC-Gbeta3 is
CC involved in the taste transduction pathway. TC-Gbeta3 may be used for
CC identifying taste modulating compounds which can be used in
CC pharmaceutical and food industries to customise taste.
XX
SQ Sequence 340 AA;

[illegible]

RESULT	9	
AABI5171		
ID	AABI5171	standard; Protein; 340 AA.
XX		
AC	AABI5171;	
XX		
DT	12-DEC-2000	(first entry)
XX		
DE	Mutant rat Taste Cell specific G-protein beta 3 subunit variant #2.	
XX		
KM	Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;	
KW	taste transduction pathway; pharmaceutical; food industry; mutation;	
KW	mutain; mutant.	
XX		
OS	Rattus sp.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 12	
FT	/note= "Wild-type Glu substituted by Asp"	
XX		
PN	WO200045179-A2.	
XX		
PD	03-AUG-2000.	
XX		
PF	26-JAN-2000; 2000WO-US02218.	
XX		
PR	27-JAN-1999; 99US-0117404.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Zuker CS, Adler JE, Lindemeier J;	
XX		
DR	WPI; 2000-499361/44.	
XX		
PT	Identifying a compound that modulates sensory signaling in sensory	
PT	cells for use in pharmaceutical and food industries comprises	
PT	contacting the compound with a sensory cell specific G-protein beta	
PT	polypeptide -	
XX		
PS	Disclosure; Page -; 68pp; English.	
XX		
CC	The present sequence is a mutant rat G-protein beta 3 subunit. G-protein	
CC	beta 3 is expressed specifically in taste cells, hence this sequence is	

CC referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3) .
 CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may
 CC be used for identifying taste modulating compounds which can be used in
 CC pharmaceutical and food industries to customise taste.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see
 CC AAB15168) and information given on page 8 of the disclosure.
 XX
 SQ Sequence 340 AA;

Query Match	97.2%	Score 1759;	DB 21;	Length 340;
Best Local Similarity	96.2%;	Pred. No. 4.8e-166;		
Matches 327;	Conservative 9;	Mismatches 4;	Indels 0;	Gaps 0;
QY 1	MGEAEOLRQEAEOQLKKQIADARRACADVTIAELVSGLEVVGROYMTRRTLRLGHLAKIYA	60		
Db 1	mgemeqqlkqeadqlkkqiadarKacacditlaelvsglevvgvymtrrtlrlghlakiya	60		
QY 61	MHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWVMTCAYAPSGNFVACGLDNM	120		
Db 61	mhwatdskllvsasqdgkllwvdyttnkvhaiplrsswvmtcayapsnfvacgldnm	120		
QY 121	CSIIYNLKSREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGPTTCALWDIETGOQKTVF	180		
Db 121	csiiyslksregnvkvsrelsahtgylscrcrflddnniwtssgpttcaldwietgqktvf	180		
QY 181	VGHTGDCMSLAVSPDFNLFISGACDASAKLWDVREGTCRQTFTHGESDINAICFPNGEA	240		
Db 181	vghtgdcmslavspdyklfisgacdasaklwdvregtcrtqtfghesdinaicffngea	240		
QY 241	ICTGSDDASCRLFLRADQELICFSHESIIGCITSVAFSLSGRLLFAGYDDFNCNWNWDSM	300		
Db 241	ictgsddascrlfldradqelictsheshiicgitsvafslsgrllfagyddfncnwnwdsi	300		
QY 301	KSERVGLSGHDNRVSCLGVTADGMAYATGSWDSFLKIWN	340		
Db 301	kservgilsghdnrsvsclgvtadgmavatsgswdsflikwn	340		

RESULT	10
AAB15172	
ID	AAB15172 standard; Protein; 340 AA.
XX	
AC	AAB15172;
XX	
DT	12-DEC-2000 (first entry)
XX	
DE	Mutant rat Taste Cell specific G-protein beta 3 subunit variant #3.
XX	
KW	Rat; Taste Cell specific G-protein beta 3 subunit; TC-Gbeta3;
KW	taste transduction pathway; pharmaceutical; food industry; mutation;
KW	muteln; mutant.
XX	
OS	Rattus sp.
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	Misc-difference 191
FT	/note= "Wild-type Ala substituted by Gly"
XX	
PN	WO200045179-A2.
XX	
PD	03-AUG-2000.
XX	
PF	26-JAN-2000; 2000WO-US02218.
XX	
PR	27-JAN-1999; 99US-0117404.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Zuker CS, Adler JE, Lindemeier J;
XX	

DR WPI; 2000-499361/44.

XX Identifying a compound that modulates sensory signaling in sensory

PT cells for use in pharmaceutical and food industries comprises

PT contacting the compound with a sensory cell specific G-protein beta

PT polypeptide -

XX

PS Disclosure; Page -, 68pp; English.

XX

CC The present sequence is a mutant rat G-protein beta 3 subunit. G-protein

CC beta 3 is expressed specifically in taste cells, hence this sequence is

CC referred to as Taste Cell specific G-protein beta 3 subunit (TC-Gbeta3).

CC TC-Gbeta3 is involved in the taste transduction pathway. TC-Gbeta3 may

CC be used for identifying taste modulating compounds which can be used in

CC pharmaceutical and food industries to customise taste.

CC Note: The present sequence is not shown in the specification but is

CC derived from the Rat wild-type TC-Gbeta3 sequence given on page 62 (see

CC AAB15168) and information given on page 8 of the disclosure.

XX

SQ Sequence 340 AA;

Query Match 97.2%; Score 1758; DB 21; Length 340;

Best Local Similarity 96.2%; Pred. No. 6.1e-166;

Matches 327; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAQLKKQIADARKACADVTLAELVSGLEVGRVQMRTRTLRGLAKIYA 60

DB 1 mgemeqlrgeaeqlkkqiadarkacadtlaelvsqlevgrvqmrtrtlrghlakiya 60

QY 61 MHMATDSKLIVSASQDGLIWDSTYTNKVHAIPLRSSWVMTCAVAPSGNFVACGGLDNM 120

DB 61 mhmatdsklivsasqdgkllwdsyttnkvhaiplrswvmtcavapsngfvacgglndm 120

QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGOQKTVF 180

DB 121 cslynlksregnvkvsrelsahthgylsccrflddnnivtssgdttcalwdietgqktvf 180

QY 181 VGHGDCMSLAVSPDENLFTSGACDASAKLMDVREGTCRQFTFGHESDINAICFPNGEA 240

DB 181 vghtgdcmslavspdenlftsgacdasaklmdvregtcrtqftghesdinaicfpngea 240

QY 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFSLGRLLFAGYDDFNCNVWDSM 300

DB 241 ictgsdascrlfdlradqelictshesicgitsvafslgrllfagyddfncnvwds1 300

QY 301 KSERVGIISGHDNRVSCIGVTADGMNAVATGSWDSFLKIWN 340

DB 301 kservgiisghdnrvscigvtadgmnavatgswdsflikwn 340

RESULT 11

AAR85859

ID AAR85859 standard; peptide; 340 AA.

XX

AC AAR85859;

XX

DT 13-SEP-1996 (first entry)

XX

DE WD-40 domain-contg. bovine G-beta-1 protein.

XX

KW WD40 repeat region; beta-transducin; protein-protein interaction; drug;

KW intracellular signaling; protein kinase C; homology; motif; modulator;

KW receptors of activated protein kinase; enzyme activity; isozyme; human.

XX

OS Bos taurus.

XX

PN W09521252-A2.

XX

PD 10-AUG-1995.

XX

PF 31-JAN-1995; 95WO-US01210.

XX

PR 01-FEB-1994; 94US-0190802.

XX

PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX

PI Mochly-Rosen D, Ron D;

XX

DR WPI; 1995-283772/37.

XX

PT New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the

PT activity of a protein, eg. protein kinase C, which interacts with a

PT protein contg. a WD-40 region.

XX

PS Example 5; Page 102-103; 351pp; English.

XX

CC Proteins AAR85851-92 are protein which contain at least one WD-40 (also

CC called beta-transducin homologous) amino acid repeat motifs. The WD-40

CC regions are involved in protein-protein interactions between proteins

CC involved in intracellular signaling. An example of such an interaction

CC is between protein kinase C and receptors of activated protein kinase

CC (RACK), esp. RACK-1 (AAR85850). Proteins AAR85851-82 were isolated based

CC on homology with beta-transducin, whereas proteins AAR85882-92 were

CC isolated based on homology with the WD-40 consensus sequence (AAR85893).

CC The proteins were used to construct the peptides AAR84928-R85063 and

CC AAR85786-R85842. The peptides can be used to identify target proteins

CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of

CC proteins involved in protein-protein interaction and to screen for drugs

CC that will affect protein-protein interaction involving WD-40 domains.

XX

SQ Sequence 340 AA;

Query Match 87.2%; Score 1578; DB 16; Length 340;

Best Local Similarity 83.2%; Pred. No. 4.2e-148;

Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAQLKKQIADARKACADVTLAELVSGLEVGRVQMRTRTLRGLAKIYA 60

DB 1 mseldqlrgeaeqlkngirdarkacadtlsqitnndpvgrygmtrtrtlrghlakiya 60

QY 61 MHMATDSKLIVSASQDGLIWDSTYTNKVHAIPLRSSWVMTCAVAPSGNFVACGGLDNM 120

DB 61 mhwtgdsrlivsasqdgkllwdsyttnkvhaiplrswvmtcavapsngnyvacgglnd1 120

QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGOQKTVF 180

DB 121 cslynlksregnvkvsrelsahthgylsccrflddnnivtssgdttcalwdietgqktvf 180

QY 181 VGHGDCMSLAVSPDENLFTSGACDASAKLMDVREGTCRQFTFGHESDINAICFPNGEA 240

DB 181 vghtgdcmslavspdenlftsgacdasaklmdvregtcrtqftghesdinaicfpngea 240

QY 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFSLGRLLFAGYDDFNCNVWDSM 300

DB 241 ictgsdascrlfdlradqelictshesicgitsvafslgrllfagyddfncnvwds1 300

QY 301 KSERVGIISGHDNRVSCIGVTADGMNAVATGSWDSFLKIWN 340

DB 301 kservgiisghdnrvscigvtadgmnavatgswdsflikwn 340

RESULT 12

AAV67863

ID AAV67863 standard; protein; 340 AA.

XX

AC AAV67863;

XX

DT 25-APR-2000 (first entry)

XX

DE Human Hgbbl G-protein betal subunit amino acid sequence.

XX

KW Ste20p/PAK; G-protein-coupled receptor signal transduction; human; Hgbbl;

KW Ste4p/Gbeta interaction domain; p21-activated protein kinase;

KW G-protein coupled receptor signal transduction;

```
XX Homo sapiens.
OS
XX CA2219958-A1.
PN
XX 07-JUL-1999.
PD
XX 07-JAN-1998; 98CA-2219958.
PF
XX 07-JAN-1998; 98CA-2219958.
PR
XX 07-JAN-1998; 98CA-2219958.
XX
XX (LEBE/) LEBERER E.
PA (LEEU/) LEEUW T.
PA (THOM/) THOMAS D Y.
PA (WHIT/) WHITEWAY M.
XX
PI Leberer E, Leeuw T, Thomas DY, Whiteway M;
XX
XX WPI; 2000-137553/13.
DR
XX
XX Interacting polypeptides involved in G-protein-coupled receptor signal
PT transduction -
XX
XX Claim 3; Fig 6; 91pp; English.
PS
XX
XX This sequence represents the beta subunit of a human G-protein. The
CC invention relates to the G-protein beta subunit interaction domain of the
CC Ste20p/PAK family of protein kinases. The Ste20p/PAK family of protein
CC kinases are p21-activated protein kinases (PAK), and they are involved in
CC many varied cellular processes ranging from morphogenesis and stress
CC response, to apoptosis. Interacting polypeptides Ste4p/Gbeta and
CC Ste20p/PAK are useful for designing in vitro and in vivo experimental
CC models which enable the screening of large collections of synthetic,
CC semi-synthetic, or natural compounds for therapeutic use in Ste4p/Gbeta
CC and Ste20p/PAK dependent diseases.
XX
XX Sequence 340 AA:
SQ
Query Match 87.2%; Score 1578; DB 21; Length 340;
Best Local Similarity 83.2%; Pred. No. 4.2e-148;
Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;
QY 1 MGEMEQLRQEAQLKKQIADARKKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
DB 1 mseldqlrgeaeqlknqirdarkacadatlsqitnnidpvgriqmrtrrlrghlakiya 60
QY 61 MHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWVMTCAVAPSGNFVACGGLDNM 120
DB 61 mhwatdsrllvasdqgkllwdsyttnkvhaiplrsswvmtcayapsgnvyacgldni 120
QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCRFLLDDNNIVTSSGDTTCALWDIETGOQKTVF 180
DB 121 cslynlktregnvrvsrelaghtgylscrrfldnnqivtssgdttcaldietgqttf 180
QY 181 VGHTGDCMSLAVSPDENLFIISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
DB 181 tghtgdvmslslapdtrlfvsgacdasaklmdvregmcrqfttghesdinaicfpngna 240
QY 241 ICTGSDDASCRLFDLRADQELICFSHESIICGITSVAFSLSGRLIFAGYDDFNCNVWDSM 300
DB 241 fatgsddatcrldfdradqelmtysdhnicgitsvfsksgrlllagyddfnncnvwdal 300
QY 301 KSERVGIILSGHDNRVSCIGVTADGMAVATGSDSFLKIWN 340
DB 301 kdragvlaghdnrsvscigvtdgmaavatgswdsflikwn 340
RESULT 13
AAW59364
ID AAW59364 standard; protein; 299 AA.
XX
AC AAW59364;
```

```
XX 10-SEP-1998 (first entry)
DT
XX Human G-protein beta-3 subunit protein.
DE
XX G protein; beta-3 subunit; human; hypertension; immunodeficient; stroke;
KW treatment; cardiovascular disease; metabolic disorder; tumour metastasis;
KW coronary heart disease; post-angioplastic re-stenosis; diabetes;
KW nephropathy; polyneuropathy; retinopathy.
XX
XX Homo sapiens.
OS
XX WO9811212-A1.
PN
XX 19-MAR-1998.
PD
XX 29-AUG-1997; 97WO-EP04709.
PF
XX 13-SEP-1996; 96DE-1037518.
PR
XX
XX (SIFERT/) SIFERT W.
PA
XX Siefert W;
PI
XX
XX WPI; 1998-271665/24.
DR N-PSDB; AAV34857.
DR
XX
XX Variant of human G protein beta-3 sub-unit - associated with
PT hypertension
XX
XX Claim 2; Page 12-13; 34pp; German.
PS
XX
XX This sequence represents a human G-protein beta-3 subunit consisting
CC of up to six WD repeat motifs (as found in hypertensive subjects, rather
CC than the seven WD repeat motifs found in normotensive subjects). The
CC nucleic acid sequence encoding this protein can be expressed in a host
CC organism to produce the protein, preferably where the host organism is an
CC immunodeficient person, especially an HIV-positive person. This sequence
CC can be used to prepare a medicament for treating diseases associated with
CC G protein mis-control e.g. cardiovascular disease, metabolic disorders or
CC immunological diseases, hypertension, coronary heart disease, stroke,
CC post-angioplastic re-stenosis, diabetic complications (e.g. nephropathy,
CC polyneuropathy or retinopathy) or tumour metastasis.
XX
XX Sequence 299 AA:
SQ
Query Match 86.2%; Score 1558.5; DB 19; Length 299;
Best Local Similarity 87.9%; Pred. No. 3e-146;
Matches 299; Conservative 0; Mismatches 0; Indels 41; Gaps 1;
QY 1 MGEMEQLRQEAQLKKQIADARKKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
DB 1 mgemeqlrgeaeqlkkqiadarkacadvtlaelvsglevgrvqmrtrrlrghlakiya 60
QY 61 MHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWVMTCAVAPSGNFVACGGLDNM 120
DB 61 mhwatdsrllvasdqgkllwdsyttnkvhaiplrsswvmtcayapsgnfyacgldnm 120
QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCRFLLDDNNIVTSSGDTTCALWDIETGOQKTVF 180
DB 121 cslynlksregnvkvsrelsahhtgylscrrfldnniivtssgdttc----- 166
QY 181 VGHTGDCMSLAVSPDENLFIISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240
DB 167 -----aklmdvregtcrtqftghesdinaicfpngea 199
QY 241 ICTGSDDASCRLFDLRADQELICFSHESIICGITSVAFSLSGRLIFAGYDDFNCNVWDSM 300
DB 200 ictgsddascrlfdlradqelicfshesicgitsvafslsgrllfagyddfnncnvwdsm 259
QY 301 KSERVGIILSGHDNRVSCIGVTADGMAVATGSDSFLKIWN 340
DB 301 kservgiilsghdnrsvscigvtadgmaavatgswdsflikwn 340
```

Db 260 kservgilsgdhnrsvclgvtadgmavatswdsfllkiwn 299

RESULT 14

AAW90939

ID AAW90939 standard; Protein: 297 AA.

AC AAW90939;

DT 14-JUL-2000 (first entry)

DE Human G-protein beta3 subunit Gbeta3s-2 protein.

Human; G-protein; beta3 subunit; anti-diabetic; cardiact; osteoporotic; obesity; hypercholesterolemia; diabetes mellitus type 2; weight; myocardial infarct; atherosclerosis; neurodegenerative; hormone therapy; cerebrovascular disease; Alzheimer's disease.

OS Homo sapiens.

PN WO200015785-A2.

PD 23-MAR-2000.

PF 06-SEP-1999; 99WO-EP06534.

PR 10-SEP-1998; 98DE-1041299.

PR 05-FEB-1999; 99DE-1004825.

PR 18-MAR-1999; 99DE-1012049.

PR 29-MAR-1999; 99DE-1014229.

PR 30-APR-1999; 99DE-1019889.

PR 21-MAY-1999; 99DE-1023539.

PA (SIFP/) SIFFERT W.

PI Siffert W;

DR WPI: 2000-271425/23.

DR N-PSDB; AAA11700.

PT A novel gene for a variant Gb3-subunit of human G-protein

PT useful for determining risk of G-protein dysfunction associated disease

PS Claim 27; Page 77-78; 78pp; German.

This invention describes novel Gbeta3-subunits of the human G-protein. The products of the invention have anti-diabetic, cardiact, osteoporotic and neuroprotective activity. Polymorphisms identified in the Gbeta3 subunit coding sequence, especially C825T and/or C1429T, can be used to identify a risk of a disease or illness associated with G-proteins dysfunction. Such diseases include diabetes mellitus type 2, excess weight and obesity, hypercholesterolemia, coronary heart disease, myocardial infarct, sudden heart death, osteoporosis, atherosclerosis, neurodegenerative or cerebrovascular diseases, in particular Alzheimer's disease, an illness based on an increased reaction of the immune system and/or a non-erectile dysfunction. The polymorphisms can also be used to predict risk in women of cardiovascular disease, in particular high blood pressure or coronary heart disease and to direct hormone therapy to reduce risk of cardiovascular risk. The sequence information can also be used to determine if there is an increased risk for HIV-positive homozygote patients of developing AIDS. An alteration in the Gbeta3-subunit, as above, can be used to identify a person with an increased CO₂- or rather a hypoxic tolerance. The polymorphism can also be used to determine the responsiveness of a patient to in vivo hormones, transmitters (also neurotransmitters) or drugs, that activate G-protein heterotrimers, which influence stimulation of G-protein subunits Gbeta3 and Gbeta3s and/or Galphas. The sequence data and methods can be used to determine specific therapies and doses for treatment of the above diseases, especially acute myocardial infarct with or without heart rhythm disturbance and transplant rejection. In particular, it can be used to predict the activity of a dose of erythropoietin on blood

formation and/or predicting the formation of hypertension under this therapy. The method can be used to predict the danger of hypertension when using immunosuppressive therapy, in particular cyclosporin. It is also possible to predict the responsiveness of a patient in vivo to a substance with prostaglandin E1 activity. Complementary sequences to the Gbeta3 subunit nucleic acid sequences can be used for antisense medicaments for therapy or prevention of disease. The Gbeta3s subunit of human G-protein can be used in a recombinant system or after transfection into a relevant cell to identify chemicals which function as inhibitors of Gbeta3s. Nucleic acid sequences encoding Gbeta3s can be used to prepare transgenic animals and to produce medicaments for treatment of misdirected G-protein associated diseases. The Gbeta3s protein can also be used to produce specific antibodies. This sequence represents the human G-protein Gbeta-3 subunit described in the method of the invention.

SQ Sequence 297 AA;

Query Match 85.6%; Score 1548.5; DB 21; Length 297; Best Local Similarity 87.4%; Pred. No. 2.9e-145; Matches 297; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MGEMEQLRQAEQQLKKQIADAKACADVTLLAELVSGLEVGRVQMRTRRLRGLAKIYA 60

Db 1 mgemeqlrqaegqlkkqladarkacadvrlaelvsglevgrvqmrtrrlrghlakiya 60

QY 61 MHWATDSKLLVSASQDGLIWDSTYTNKVAIPLRSSWMTCAYPASGNEVACGLDMM 120

Db 61 mhwatdskllvsasqdgkllwdsyttnkvaiprlsswmtcayapsngnevacgldmm 120

QY 121 CSTYNLKSRREGVNVKVSRELSAHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQKTVF 180

Db 121 cstynlksregvntvksrelshahgytscrfllddnnivtssgdttcaldietgqktvf 180

QY 181 VGHGTGDCMSLAVSPDENLFISGACDASAKLMDVREGTCROTFTGHESDINAICFPNGEA 240

Db 181 vghtgdcmslavspdfnlfisgacdasaklmdvregtcrotftghesdinaicfpngea 240

QY 241 ICTGSDASCRFLDLRADELICFSESIIICGITSVAFLSGRLFPAGYDDFNCNVWDSM 300

Db 235 -----fslsgrlflfagydffncnvwds 257

QY 301 KSERVGLSGHNDNRVSLGVTADGMVAATGWSWDSFLKIWN 340

Db 258 kservgilsgdhnrsvclgvtadgmavatswdsfllkiwn 297

RESULT 15

AAW85863

ID AAW85863 standard; peptide: 340 AA.

AC AAW85863;

DT 13-SEP-1996 (first entry)

DE WD-40 domain-contg. human G-beta-2 protein.

WD40 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signaling; protein kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.

OS Homo sapiens.

PN WO9521252-A2.

PD 10-AUG-1995.

PF 31-JAN-1995; 95WO-US01210.

PR 01-FEB-1994; 94US-0190802.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

Fri Sep 28 10:45:11 2001

PI Mochly-Rosen D, Ron D;

XX WPI; 1995-283772/37.

XX New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
PT activity of a protein, eg. protein kinase C, which interacts with a
PT protein contg. a WD-40 region.

XX Example 5; Page 109-110; 351pp; English.

XX Proteins AAR85851-92 are protein which contain at least one WD-40 (also
CC called beta-transducin homologous) amino acid repeat motifs. The WD-40
CC regions are involved in protein-protein interactions between proteins
CC involved in intracellular signalling. An example of such an interaction
CC is between protein kinase C and receptors of activated protein kinase
CC (RACK), esp. RACK-1 (AAR85850). Proteins AAR85851-82 were isolated based
CC on homology with beta-transducin, whereas proteins AAR85882-92 were
CC isolated based on homology with the WD-40 consensus sequence (AAR85893).
CC The proteins were used to construct the peptides AAR84928-R85063 and
CC AAR85786-R85842. The peptides can be used to identify target proteins
CC contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of
CC proteins involved in protein-protein interaction and to screen for drugs
CC that will affect protein-protein interaction involving WD-40 domains.

XX Sequence 340 AA;

Query Match 84.5%; Score 1528; DB 16; Length 340;
Best Local Similarity 80.9%; Pred. No. 3.8e-143;
Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGEMQLROAEQLKKQIADARKACADVTLAELVSGLEVGRVOMRRRTLRLGLAKIYA 60
Db 1 mselqlrqaeeqlnqirdarkacgdstltqtagldpvgrlqmrtrrlrhlakiya 60
QY 61 MHWATDSKLVASQDGLIWMDSYTTNKVHAIPLRSSWMTCAYPASGNFVACGGLDNM 120
Db 61 mhwatdsrllvsasqdgkllwdsytltnkvhaiplrswmtcayapsgnfvaacgldni 120
QY 121 CSTYNLKSREGNVKVSRELTAHTGYLSCCRPLDDNNIVTSSGDTTCALWDIETGQKTVF 180
Db 121 csylsktregnvrsreltpgltgylscrrfldnqiltssgdttcaldietgqktvf 180
QY 181 VGHGTDCMSLAVSPDFNLFIGACDASAKIMDVRECTCROTFTHESDINAICFPNGEA 240
Db 181 aghsgdvmslslapdgrtfvsgacdasiklwdvrdsmcrtffignesdinavafpnyga 240
QY 241 ICTGSDDASCRLFDLRADQELICSHESIICGITSVAFSLGRLTFAGYDDFNCNVWDSM 300
Db 241 ftgsddatcrlfdlradeqellmshndhlcgitsvafsrgrlllagyddfnclwadam 300
QY 301 KSERVGLSGHDNRVSCIGVTADGMVATGSMDSFLKIMN 340
Db 301 kgdragvlaghdnrsvclgvtddgmavatswdsflkiwn 340

Search completed: September 28, 2001, 10:29:22
Job time: 72 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:28:39 ; Search time 20.71 Seconds
(without alignments)
338.036 Million cell updates/sec

Title: US-09-492-029-5
Perfect score: 1809
Sequence: 1 MGEMEQLRQAEQKQIAD.....TADGMAVATGSGWDSFLKIWN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1809	100.0	340	4	US-09-180-783-2 Sequence 2, Appli
2	1578	87.2	340	1	US-08-190-802A-38 Sequence 38, Appli
3	1558.5	86.2	299	4	US-09-147-826B-2 Sequence 2, Appli
4	1528	84.5	340	1	US-08-190-802A-42 Sequence 42, Appli
5	1463	80.9	340	1	US-08-190-802A-45 Sequence 45, Appli
6	1459	80.7	340	1	US-08-190-802A-40 Sequence 40, Appli
7	1421	78.6	326	1	US-08-190-802A-39 Sequence 39, Appli
8	949.5	52.5	395	3	US-09-032-372-1 Sequence 1, Appli
9	650	35.9	423	1	US-08-190-802A-61 Sequence 61, Appli
10	305.5	16.9	317	1	US-08-190-802A-27 Sequence 27, Appli
11	305.5	16.9	317	1	US-08-190-802A-41 Sequence 41, Appli
12	305.5	16.9	317	1	US-08-190-802A-47 Sequence 47, Appli
13	296	16.4	704	1	US-08-190-802A-62 Sequence 62, Appli
14	296	16.4	704	1	US-08-188-582-5 Sequence 5, Appli
15	296	16.4	704	1	US-08-646-715-5 Sequence 5, Appli
16	296	16.4	704	2	US-08-308-818-3 Sequence 3, Appli
17	287	15.9	587	3	US-08-899-578-2 Sequence 2, Appli
18	274	15.1	704	3	US-08-188-582-18 Sequence 18, Appli
19	274	15.1	704	1	US-08-646-715-18 Sequence 18, Appli
20	271.5	15.0	439	1	US-08-190-802A-65 Sequence 65, Appli
21	265	14.6	318	1	US-08-190-802A-33 Sequence 33, Appli
22	257.5	14.2	514	1	US-08-190-802A-66 Sequence 66, Appli
23	251	13.9	798	1	US-08-190-802A-64 Sequence 64, Appli
24	251	13.9	798	1	US-08-190-802A-68 Sequence 68, Appli
25	247	13.7	713	1	US-08-308-818-2 Sequence 2, Appli
26	247	13.7	713	1	US-08-190-802A-63 Sequence 63, Appli
27	242	13.4	375	4	US-09-063-743-1 Sequence 1, Appli

28	241.5	13.3	343	4	US-09-063-743-5	Sequence 5, Appli
29	239	13.2	305	3	US-08-965-600-1	Sequence 1, Appli
30	237	13.1	409	2	US-08-283-917-3	Sequence 3, Appli
31	237	13.1	409	2	US-08-961-716-3	Sequence 3, Appli
32	237	13.1	410	2	US-08-283-917-9	Sequence 9, Appli
33	237	13.1	410	2	US-08-961-716-9	Sequence 9, Appli
34	231.5	12.8	906	1	US-08-190-802A-31	Sequence 31, Appli
35	227.5	12.6	409	1	US-08-190-802A-51	Sequence 51, Appli
36	212.5	11.7	2627	2	US-08-751-189-3	Sequence 3, Appli
37	212.5	11.7	2627	2	US-09-060-836-3	Sequence 3, Appli
38	212.5	11.7	2627	4	US-09-184-445-3	Sequence 3, Appli
39	210	11.6	517	1	US-08-190-802A-30	Sequence 30, Appli
40	209	11.6	2629	2	US-08-751-189-4	Sequence 4, Appli
41	209	11.6	2629	2	US-09-060-836-4	Sequence 4, Appli
42	209	11.6	2629	4	US-09-184-445-4	Sequence 4, Appli
43	203.5	11.2	597	2	US-08-883-534-6	Sequence 6, Appli
44	203.5	11.2	597	3	US-09-204-764-6	Sequence 6, Appli
45	197.5	10.9	376	2	US-08-883-534-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-180-783-2
Sequence 2, Application US/09180783
Patent No. 6242181
GENERAL INFORMATION:
APPLICANT: Sifert, Winfried
TITLE OF INVENTION: THE USE OF A GENETIC MODIFICATION IN THE GENE FOR HUMAN
FILE REFERENCE: 1135-2
CURRENT APPLICATION NUMBER: US/09/180,783
CURRENT FILING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: PCT/EP97/02250
PRIOR FILING DATE: 1997-05-02
PRIOR APPLICATION NUMBER: DE 19619362.1
PRIOR FILING DATE: 1996-05-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-09-180-783-2

QY	1	MGEMEQLRQAEQKQIADARKACADVTIAELVSGLEVGRVQMRTRTLRGLAKIYA	60
DB	1	MGEMEQLRQAEQKQIADARKACADVTIAELVSGLEVGRVQMRTRTLRGLAKIYA	60
QY	61	MHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAIAPSGNFVACGGLDM	120
DB	61	MHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAIAPSGNFVACGGLDM	120
QY	121	CSIYNLKSREGNVKVSRELSTHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQKTYF	180
DB	121	CSIYNLKSREGNVKVSRELSTHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQKTYF	180
QY	181	VGHTGDCMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTGHSIDINACFFPNGEA	240
DB	181	VGHTGDCMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTGHSIDINACFFPNGEA	240
QY	241	ICTGSDDASCRLFDLRADQLICFHSIICGITSVAFLSGRLLFAGYDFFNCNVWDSM	300
DB	241	ICTGSDDASCRLFDLRADQLICFHSIICGITSVAFLSGRLLFAGYDFFNCNVWDSM	300
QY	301	KSERVGLSGHDNRVSCIGVTADGMAVATGSGWDSFLKIWN	340
DB	301	KSERVGLSGHDNRVSCIGVTADGMAVATGSGWDSFLKIWN	340

Db 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGSDSFLKIWN 340

RESULT 2

US-08-190-802A-38
Sequence 38, Application US/08190802A
Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G-Beta 1 bovine, Fig. 21

US-08-190-802A-38

Query Match

Best Local Similarity 87.2%; Score 1578; DB 1; Length 340;
Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGEMQLRQAEQKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
DB 1 MSELQDLRQAEQKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
QY 61 MHMATDSKLVSASQDGLIYWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
DB 61 MHMATDSKLVSASQDGLIYWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSTYNLKSREGNVKVSRELSTHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQKTVF 180
DB 121 CSTYNLKSREGNVKVSRELSTHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQKTVF 180
QY 181 VGHGDCMSLAVSPDFNLISGACDASAKLMDVREGTCRQFTGHESDINAIKCFPNGEA 240
DB 181 VGHGDCMSLAVSPDFNLISGACDASAKLMDVREGTCRQFTGHESDINAIKCFPNGEA 240
QY 241 ICTGSDDASCRLFDLRADQELICFSHESIICGITSVAFSLGRLLFAGYDDFNQVWDSM 300
DB 241 FATGSDATCRLFDLRADQELICFSHESIICGITSVAFSLGRLLFAGYDDFNQVWDSM 300

QY

301 KSERVGLSGHNDNRVSCIGVTADGMAVATGSDSFLKIWN 340

Db

301 KADRAGVLGHNDNRVSCIGVTDDGMAVATGSDSFLKIWN 340

RESULT 3

US-09-147-826B-2

Sequence 2, Application US/09147826B
Patent No. 6251853

GENERAL INFORMATION:

APPLICANT: Siffert, Winfried
TITLE OF INVENTION: PTX-SENSITIVE G PROTEINS, THEIR PREPARATION AND USE
FILE REFERENCE: 1135-0003
CURRENT APPLICATION NUMBER: US/09/147,826B
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: PCT/EP97/04709
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: DE 196 37 518.5
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens

US-09-147-826B-2

Query Match

Best Local Similarity 86.2%; Score 1558.5; DB 4; Length 299;
Matches 299; Conservative 0; Mismatches 0; Indels 41; Gaps 1;

QY 1 MGEMQLRQAEQKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
DB 1 MGEMQLRQAEQKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
QY 61 MHMATDSKLVSASQDGLIYWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
DB 61 MHMATDSKLVSASQDGLIYWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSTYNLKSREGNVKVSRELSTHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQKTVF 180
DB 121 CSTYNLKSREGNVKVSRELSTHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQKTVF 180
QY 181 VGHGDCMSLAVSPDFNLISGACDASAKLMDVREGTCRQFTGHESDINAIKCFPNGEA 240
DB 181 VGHGDCMSLAVSPDFNLISGACDASAKLMDVREGTCRQFTGHESDINAIKCFPNGEA 240
QY 241 ICTGSDDASCRLFDLRADQELICFSHESIICGITSVAFSLGRLLFAGYDDFNQVWDSM 300
DB 241 ICTGSDDASCRLFDLRADQELICFSHESIICGITSVAFSLGRLLFAGYDDFNQVWDSM 300
QY 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGSDSFLKIWN 340
DB 260 KSERVGLSGHNDNRVSCIGVTADGMAVATGSDSFLKIWN 299

RESULT 4

US-08-190-802A-42

Sequence 42, Application US/08190802A
Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA

STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GTP binding protein (squid), Fig. 28

Query Match	80.9%;	Score 1463;	DB 1;	Length 341;
Best Local Similarity	79.0%;	Pred. No. 3e-137;		

QY	3	EMEO LRQEA EOLK KOIADARKACADVTLAE LVSGLEVNGRYOMTRRTLGRHLAKIYAMH	62
Db	4	ELFALRQETEO LKNQ IREARKAAADTTLAMATANVEPVGRIOMTRRTLGRHLAKIYAMH	63
QY	63	WATDSKLLVSASODGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNMCS	122
Db	64	WASDSRNLVSASODGKLIWMDGYTTNKVHAIPLRSSWMTCAVAPSGNYVACGGLDNICS	123
QY	123	IYNLKSREGNVKVSREL SAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGOOKTYVVG	182
Db	124	IYSLKTRREGNVKVSRELPGHTGYLSCCRFLDDNQIVTSSGDMTCALMNIETGNQITSFEG	183
QY	183	HTGDCMSLAVSPDENLEISGACDASAKLMDVREGTCROTFTGHESDINAI CFFPNGEAIC	242
Db	184	HTGDVMSLSLAPDMRTFVSGACDASAKLFDLRDGI CQTFTGHESDINAI TFFPNGEAFA	243
QY	243	TGSDDASCRFLDLRADQELICFSHESIICGITSVAFSLSGRLLFAGYDDFENCNVWDSMKS	302
Db	244	TGSDDATCRLFLDIRADQETIGMYSHDNITICGITSVAFSKSGRLLLGTYDDFENCNVMDVLKQ	303
QY	303	ERYGILSGHDNRVSC LGVTADGMAVATGSWDSFLKIWN	340
Db	304	ERAGVLAGHDNRVSC LGVTEDEGMAVATGSWDSFLKIWN	341

```

RESULT      6
US-08-190-802A-40
; Sequence 40, Application US/08190802A
; Patent No. 5519003
;
; GENERAL INFORMATION:
;
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Dehlinger & Associates
;

```

STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G- BETA DROSOPH, Fig. 23
US-08-190-802A-40

Query Match 80.7%; Score 1459; DB 1; Length 340;
Best Local Similarity 77.4%; Pred. No. 7.6e-137;
Matches 263; Conservative 35; Mismatches 42; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAQKQIADARACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
DB 1 MNELSLRQEAESLKNARIDARACADTSLQAATSLERIGRIQMRTRRLRGLAKIYA 60
QY 61 MHWAIDSKLLVSASQDGLIYWDSTYTNKVHAIPLRSSWMTCAIAPSGNFVACGGGLDM 120
DB 61 MHWGNDNRNLVSASQDGLIYWDSTYTNKVHAIPLRSSWMTCAIAPSGNFVACGGGLDM 120
QY 121 CSIYNLKSREGNVKVSRELSTHTGYSLSRFLDNNITVSSGDTTCALWDIETGQOKTVF 180
DB 121 CSIYNLKTREGNVKVSRELSTHTGYSLSRFLDNNITVSSGDTTCALWDIETGQOKTVF 180
QY 181 VGHGDCMSLAVSPDNLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
DB 181 LGHTGDYMALSLAPQCKTFVSGACDASAKLMDIREGVCKOTFPGHESDINAVTFPPNGQA 240
QY 241 ICTGSDDASCRFLDLRADQELICFSHESIIGTISVAFSLSGRLTFAGYDDFNCNVWDSM 300
DB 241 FATGSDDATCRFLDFIRADQELAMYSHDNIICGITSVAFSKSGRLLAGYDDFNCNVWDSM 300
QY 301 KSERVGLSGHNRVSCIGVTADGMAVATGSDSFLKIWN 340
DB 301 KAERSGILAGHDNRVSCIGVTENGMAVATGSDSFLRWN 340

RESULT 7
US-08-190-802A-39
Sequence 39, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theeof
NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G-Beta- bovine (2), Fig. 22
US-08-190-802A-39

Query Match 78.6%; Score 1421; DB 1; Length 326;
Best Local Similarity 78.2%; Pred. No. 4.2e-133;
Matches 259; Conservative 29; Mismatches 33; Indels 10; Gaps 2;

QY 15 KQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYAMHWATDSKLLVSAS 74
DB 1 RNQIRDARKACAGDSTLQITAGLDPVGRIGMRTRRLRGLAKIYAMHWATDSKLLVSAS 60
QY 75 QDGLIWDSTYTNKVHAIPLRSSWMTCAIAPSGNFVACGGGLDMCSYMLKSR 129
DB 61 QDGLIWDSEGNVRYTTNKVHAIPLRSSWMTCAIAPSGNFVACGGGLDMCSYMLKSR 120
QY 130 EGNVKSRELSTHTGYSLSRFLDNNITVSSGDTTCALWDIETGQOKTVFVGHGDCMS 189
DB 121 -----VSRELPGHTGYSLSRFLDNNITVSSGDTTCALWDIETGQOKTVFVGHGDCMS 175
QY 190 LAVSPDNLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEAICTGSDAS 249
DB 176 LSLAPDGRFTVSGACDASIKLMDVDRSMCROTFTGHESDINAVAFPPNGYAFITGSDAT 235
QY 250 CRLFLRADQELICFSHESIIGTISVAFSLSGRLTFAGYDDFNCNVWDSMKSERVGLS 309
DB 236 CRLFLRADQELIMYSHDNIICGITSVAFSRSRGLLAGYDDFNCNIMWDMKDRAGVLA 295
QY 310 GHDNRVSCIGVTADGMAVATGSDSFLKIWN 340
DB 296 GHDNRVSCIGVTDDGMAVATGSDSFLKIWN 326

RESULT 8
US-09-032-372-1
Sequence 1, Application US/09032372
Patent No. 6008337
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.

	Query Match	52.5%;	Score 949.5;	DB 3;	Length 395;
	Best Local Similarity	52.2%;	pred. No. 3.5e-86;		
	Matches 178;	Conservative	56;	Mismatches 102;	Indels 5; Gaps 3;
Qy	4 MEQLRQEAQLKKQIADARKACADVTYLAELVSGLEVVGRYQMRTRTLRGHLAKIYAMHW	63			
Db	54 LASLKEAEESLKGKLEERAKLHVDYELHQVAERVEALGQFYMKTRRTLKGHGKYLCDMW	113			
Qy	64 ATDSKLLVASQDCKLIWDSYTNKVAHPILRSSWMTCAIAPSGNFVACGGDLNMCIS	123			
Db	114 CKDKRRIVSSSDGKVIWDSFTTNKEHAVTMPTWMACAYAPSGCAIACGGDLNKCYS	173			
Qy	124 YNL--KSREGNAVVSRELSAHTGYLSCCRFLD-DNNIVTSSGPTTCALMDIETGQKTVF	180			
Db	174 YPLTFDKNNMAKKKSVAAMHTNYLSACSTTNSDMQILTLASGDGTCALMDVESGQLQSF	233			
Qy	181 VGHGTGD-CMSLAVSPDENLFIGACDASAKIMDVREGTCRQFTGHESDINAIICFPNG	238			
Db	234 HGHGADVLCILDAPSETGNTFVSGGCDKKAMVDMRSGQCVOAFETHESDINSVRYPPSG	293			
Qy	239 EAICTGSDDASCRLFDLRADQELICFSHESITIGITSVAFSLSGRLLEAGYDDFNCNVMD	298			
Db	294 DAFASGSDDATCRLYDLRADRERVAIYSKESITIFGASSVDVDFSLSGRLLEAGYNDYTIWMD	353			
Qy	299 SMKSERVGIILSGHDNRVSCIGVTADGMAVATGSDWSFLKIW	339			
Db	354 VLKGSRYILFGHENRVSTLRVSPDGTAFCSGSGSWDHTLRW	394			

Query Match	35.9%;	Score 650;	DB 1;	Length 423;
Best Local Similarity	36.8%;	Pred. No. 2.1e-56;		
Matches 141;	Conservative	71;	Mismatches 125;	Indels 46;
				Gaps
QY	3	EMEQLRQEAEOIKQIADARKACADVTYLAELVSGLEV--GRVQMRTRRTLGRHLAKIYA	60	
DB	38	KIEARQESKQIHAQINAKAKHIQDASLFEQANKVTSLTQKINLKNIVLKGHNKISD	97	
QY	61	MHWATDSKLLVASASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGIDNM	120	
DB	98	FRMSRDSKRILSASQDGEFWLIWDSASGLKQNAIPLDSQWVLSCAISPSSTLVASAGLNN	157	
QY	121	CSITNLKSRGNV--KVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGOOKT	178	
DB	158	CTIYRV-SKENRVAQNVASTFEGHTCYISDIEFTDNAHILITASGDMTCALMDIPKAKRVR	216	
QY	179	VEVGHGTDCMSLAVSPDFNL-----FISGACDASAKIMDVREGTCRQITFTGHESDINAI	232	
DB	217	EYSDHLGDLVALAIPPEPNLENSNTFEASCGSDGYTYIWDSPSAVSQSEYVNDSDINAL	276	
QY	233	CEFPNGEALCTGSDDASCRLFDLRADQELICFS-----	265	
DB	277	RFFKDGMSIYAGSDNGAIIIMYDLRSDCIATFSLFRGYEERTPTPTYYMAANNEYNTAOSP	336	
QY	266	-----HESIT--CGITSVAFLSGRLLEAGYDDFNCAVWDSMKSERVIGILSGHDNRVSC	317	
DB	337	QTLKSTSSSYLDNQGVSLDFASGRLMYSCYTTDIGNVAVDYLKGEIVGKLEGHGGRVTG	396	

QY 318 LGVTADGMAVATGSDWSEFLKIWN 340
 Db 397 VRSSPDGLAVCTGSDWSTMKIWS 419

RESULT 10

US-08-190-802A-27
 ; Sequence 27, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: Thereof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190,802A
 ; FILING DATE: 01-FEB-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 8600-0139
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 317 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: RACK1 Amino Acid Sequence, Fig. 1C
 ; US-08-190-802A-27

Query Match 16.9%; Score 305.5; DB 1; Length 317;
 Best Local Similarity 31.5%; Pred. No. 2.2e-22;
 Matches 82; Conservative 45; Mismatches 118; Indels 15; Gaps 6;

QY 48 RRTLRGHLAKIYAMHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAP 107
 Db 56 QRALRGHSHFVSDVVISDGFALSGSWDGLRLWDLTTGTTTTRRFVGHGHTKDVLSVAFSS 115
 QY 108 SGNFYACGGGLDNMCSIYNLKSREGNVKVSRELSAHTGYLSCCRFL--DDNNIVTSSG-DT 164
 Db 116 DNRQIVSGSRDKTIKLMNTL---GVCKYTVQDESHSEWVSCVRFSPNSSNPILIVSCGWDK 172
 QY 165 TCALWDIETGQOKTVFVGHGTGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCRQFTG 224
 Db 173 LVKVMNLANCKLKTNHGHTGYLNTVTVSPDGLCASGKGQAMLMWDLNEGKHLTYLDG 232
 QY 225 HESDINAIICEFPNGEAICTGSDDASCRLFLRA-----DQELICFSHESIIGITSVA 277
 Db 233 GDI-INALCFSPNRYWLCAAT-GPSIKIWDLEGIIVDELKQEVISTSSKAEPPOCTSLA 290
 QY 278 FSLSGRLLFAGYDDFNCNVW 297

Db 291 WSADGQTLFAGYTDNLVVRW 310

RESULT 11

US-08-190-802A-41
 ; Sequence 41, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: Thereof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190,802A
 ; FILING DATE: 01-FEB-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 8600-0139
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 317 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: G-BETA HUMAN, Fig. 24
 ; US-08-190-802A-41

Query Match 16.9%; Score 305.5; DB 1; Length 317;
 Best Local Similarity 31.5%; Pred. No. 2.2e-22;
 Matches 82; Conservative 45; Mismatches 118; Indels 15; Gaps 6;

QY 48 RRTLRGHLAKIYAMHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAP 107
 Db 56 QRALRGHSHFVSDVVISDGFALSGSWDGLRLWDLTTGTTTTRRFVGHGHTKDVLSVAFSS 115
 QY 108 SGNFYACGGGLDNMCSIYNLKSREGNVKVSRELSAHTGYLSCCRFL--DDNNIVTSSG-DT 164
 Db 116 DNRQIVSGSRDKTIKLMNTL---GVCKYTVQDESHSEWVSCVRFSPNSSNPILIVSCGWDK 172
 QY 165 TCALWDIETGQOKTVFVGHGTGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCRQFTG 224
 Db 173 LVKVMNLANCKLKTNHGHTGYLNTVTVSPDGLCASGKGQAMLMWDLNEGKHLTYLDG 232
 QY 225 HESDINAIICEFPNGEAICTGSDDASCRLFLRA-----DQELICFSHESIIGITSVA 277
 Db 233 GDI-INALCFSPNRYWLCAAT-GPSIKIWDLEGIIVDELKQEVISTSSKAEPPOCTSLA 290
 QY 278 FSLSGRLLFAGYDDFNCNVW 297
 Db 291 WSADGQTLFAGYTDNLVVRW 310

US-08-190-802A-47

```

RESULT 13
US-08-190-802A-62
; Sequence 62, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: Wd-40 - Derived Peptides and Uses
; TITLE OF INVENTION: thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: TRANSCRIPTION FACTOR T11F, Fig. 45
US-08-190-802A-62

```

US-08-190-802A-62

[illegible]

Fri Sep 28 10:45:11 2001

us-09-492-029-5.rai

Page 9

Db 454 YRCAFAPEMNLISCSEDSTIRLWSLLTWSCVVTYRGHVYPWVDVRFAPHGYFVSCSYD 513
QY 206 ASAKLMDVREGTCRQFTGHESDINAICFPNGEACTGSDDASCRLFDLRADQEL-ICF 264
Db 514 KTARLWATDSNOALRVFVGHLSVDVCVQFHPNSNYVATGSSDRFVRLMDNMTGOSVRLMT 573
QY 265 SHESIICGITSVAFSLSGRLIFAGYDDFNCNVWDSMKSERVGIISGHDNRSVCLGVTADG 324
Db 574 GHKG--SVSSLAFSACGRYLASGSVDHNIIIMDLNSGSLVTTLLRHRSTVTTITFSRDG 630
QY 325 MAVATGSWDSFLKIWN 340
Db 631 TVLAAAGLDNNLTLMWD 646

Search completed: September 28, 2001, 10:28:40
Job time: 31 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:33:20 ; Search time 25.94 seconds
(without alignments)
998.433 Million cell updates/sec

Title: US-09-492-029-5
Perfect score: 1809
Sequence: 1 MGEMEQLRQEAQLKKQIAD.....TADGMVAATGWSDFLKIWN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*

1: pirl:1:1
2: pirl:2:1
3: pirl:3:1
4: pirl:4:1

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1809	100.0	340	1 RGHUB3	GTP-binding regula
2	1762	97.4	340	2 T53871	G-protein beta-sub
3	1578	87.2	340	1 RGHUB1	GTP-binding regula
4	1578	87.2	340	1 RGHOB1	GTP-binding regula
5	1578	87.2	340	2 JC5057	G protein beta 1 -
6	1528	84.5	340	1 RGHUB2	GTP-binding regula
7	1525	84.3	340	2 T20830	hypothetical prote
8	1520	84.0	340	1 RGHUB	GTP-binding regula
9	1500	82.9	340	1 RGHUB4	GTP-binding regula
10	1480	81.8	341	2 S34348	GTP-binding regula
11	1469	81.2	326	1 RGHOB2	GTP-binding regula
12	1463	80.9	341	1 RGHOB	GTP-binding regula
13	1459	80.7	340	1 RGHOBH	GTP-binding regula
14	1238	68.4	347	2 A47370	beta-5 GTP-binding
15	948.5	52.4	353	2 A54969	hypothetical prote
16	927.5	51.3	356	2 T22478	GTP-binding regula
17	847	46.8	380	2 T03765	GTP-binding regula
18	831	45.9	380	2 T02085	GTP-binding regula
19	824	45.6	377	2 T04086	GTP-binding regula
20	822	45.4	375	2 T03256	GTP-binding regula
21	822	45.4	377	2 T04089	GTP-binding regula
22	822	45.4	346	1 RGHOB	GTP-binding regula
23	817	45.2	377	2 T05266	GTP-binding regula
24	815	45.1	380	2 T08036	GTP-binding regula
25	794	43.9	377	2 T16985	GTP-binding regula
26	790	43.7	283	2 T17256	hypothetical prote
27	743.5	41.1	317	2 S72457	GTP-binding regula
28	670	37.0	305	2 T50474	GTP-binding regula
29	668	36.9	305	2 T50474	GTP-binding regula

30	647	35.8	423	2	S60939	GTP-binding protei
31	609	33.7	123	2	S29121	GTP-binding regula
32	585.5	32.4	240	2	T02059	GTP-binding regula
33	377.5	20.9	1356	2	T18521	beta transducin-1i
34	308.5	17.1	465	2	A32569	probable WD-repeat
35	308	17.0	333	2	G85034	GTP-binding protei
36	305.5	16.9	317	2	A33928	GTP-binding regula
37	305.5	16.9	317	2	B33928	GTP-binding regula
38	305.5	16.9	317	2	S45054	GTP-binding regula
39	305.5	16.9	317	2	S38398	activated protein
40	305.5	16.9	502	2	T41148	trp-asp repeat con
41	305.5	16.9	586	2	T38992	WD-40 repeat regul
42	300.5	16.6	1693	2	S76086	beta transducin-1i
43	299.5	16.5	1049	2	T42045	beta transducin-1i
44	299	16.5	554	2	T02445	probable U4/U6 sma
45	297	16.4				

ALIGNMENTS

RESULT 1

RGHUB3

GTP-binding regulatory protein beta-3 chain - human

N;Alternate names: guanine nucleotide binding protein beta-3 chain; heterotrimeric G-

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C;Accession: A35096

R;Levine, M.A.; Smallwood, P.M.; Moen Jr., P.T.; Helman, L.J.; Ahn, T.G.

Proc. Natl. Acad. Sci. U.S.A. 87, 2329-2333, 1990

A;Title: Molecular cloning of beta3 subunit, a third form of the G protein beta-subun

A;Reference number: A35096; MUID:90192801

A;Accession: A35096

A;Molecule type: mRNA

A;Residues: 1-340 <LEV>

A;Cross-references: GB:M31328; NID:q183412; PIDN:AA52582.1; PID:q306776

C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that re

ains. The beta and gamma chains, required for GTPase activity, appear to be common to

rase; it is specific for each type of G protein.

C;Comment: In mammals, four distinct types of beta chains have been found.

C;Genetics:

A;Gene: GDB:GNB3

A;Cross-references: GDB:120005; OMIM:139130

A;Map position: 12p13-12p13

C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C;Keywords: GTP binding; heterotrimer; signal transduction

F;51-84/Domain: WD repeat homology <WD1>

F;88-126/Domain: WD repeat homology <WD2>

F;139-171/Domain: WD repeat homology <WD3>

F;180-213/Domain: WD repeat homology <WD4>

F;222-255/Domain: WD repeat homology <WD5>

F;263-299/Domain: WD repeat homology <WD6>

F;308-340/Domain: WD repeat homology <WD7>

Query Match	100.0%;	Score 1809;	DB 1;	Length 340;
Best Local Similarity	100.0%;	Pred. No. 7.5e-145;		
Matches 340;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Db	1	MGEMEQLRQEAQLKKQIADARACADVTTLAEVSGLEVVGVRVQMRRTTLRGLAKIYA	60	
Qy	1	MGEMEQLRQEAQLKKQIADARACADVTTLAEVSGLEVVGVRVQMRRTTLRGLAKIYA	60	
Db	61	MHWATDSKLVASASQDGLIWDSTYTNKVAIPLRSSVMTCAYAPSGNFVACGLDNM	120	
Qy	61	MHWATDSKLVASASQDGLIWDSTYTNKVAIPLRSSVMTCAYAPSGNFVACGLDNM	120	
Db	121	CSLYNLKSRGNVKSRELSTHTGYSCTCRFLDDNNITVSSGDTTCALMDIETGOQKTVF	180	
Qy	121	CSLYNLKSRGNVKSRELSTHTGYSCTCRFLDDNNITVSSGDTTCALMDIETGOQKTVF	180	
Db	121	CSLYNLKSRGNVKSRELSTHTGYSCTCRFLDDNNITVSSGDTTCALMDIETGOQKTVF	180	
Qy	121	CSLYNLKSRGNVKSRELSTHTGYSCTCRFLDDNNITVSSGDTTCALMDIETGOQKTVF	180	
Db	181	VGHGDCMSLAVSPDFNLTSGACDASAKIMDVREGTCRQTFTGHESDINATGFPNGEA	240	
Qy	181	VGHGDCMSLAVSPDFNLTSGACDASAKIMDVREGTCRQTFTGHESDINATGFPNGEA	240	

Db 181 VGHGDCMSLAVSPDENLFIISGACDASAKLMDVREGTCRQFTGHESDINAICFFPNGEA 240
QY 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFLSGLRLLFAGYDDFNWDSM 300
Db 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFLSGLRLLFAGYDDFNWDSM 300
QY 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGWSWDSFLKIWN 340
Db 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGWSWDSFLKIWN 340

RESULT 2

153871
G-protein beta-subunit - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C:Accession: I53871
R:Ray, K.; Robishaw, J.D.
Gene 149, 337-340, 1994
A:Title: Cloning and sequencing of a rat heart cDNA encoding a G-protein beta subunit re
A:Reference number: I53871; MUID:95047499
A:Accession: I53871
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-340 <RES>
A:Cross-references: GB:L29090; NID:g456703; PIDN:AAA62620.1; PID:g456704
C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
F:222-255/Domain: WD repeat homology <WDR>

Query Match 97.4%; Score 1762; DB 2; Length 340;
Best Local Similarity 96.5%; Pred. No. 6.8e-141;
Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAELKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
Db 1 MGEMEQLRQEAELKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
QY 61 MHMATDSKLVASASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGLDNN 120
Db 61 MHMATDSKLVASASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGLDNN 120
QY 121 CSIYNLKSREGNVKVSRELTAHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQOKTVE 180
Db 121 CSIYNLKSREGNVKVSRELTAHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQOKTVE 180
QY 181 VGHGDCMSLAVSPDENLFIISGACDASAKLMDVREGTCRQFTGHESDINAICFFPNGEA 240
Db 181 VGHGDCMSLAVSPDENLFIISGACDASAKLMDVREGTCRQFTGHESDINAICFFPNGEA 240
QY 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFLSGLRLLFAGYDDFNWDSM 300
Db 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFLSGLRLLFAGYDDFNWDSM 300
QY 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGWSWDSFLKIWN 340
Db 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGWSWDSFLKIWN 340

RESULT 3

RGHUB1
GTP-binding regulatory protein beta-1 chain - human
N:Alternate names: guanine nucleotide binding protein beta-1 chain; heterotrimeric G-
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C:Accession: A24853
R:Codina, J.; Stengel, D.; Woo, S.L.C.; Birnbaumer, L.
FEBS Lett. 207, 187-192, 1986
A:Title: Beta-subunits of the human liver Gs/Gi signal-transducing proteins and those of
A:Reference number: A91368; MUID:87030912
A:Accession: A24853
A:Molecule type: mRNA
A:Residues: 1-340 <COD>

A:Cross-references: GB:X04526; NID:g31667; PIDN:CAA28207.1; PID:g31669
A:Experimental source: Liver
A:Note: The authors translated the codon GAG for residues 138 and 172 as Gln
C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
ase; it is specific for each type of G protein.
C:Comment: In mammals, four distinct types of beta chains have been found.
C:Genetics:
A:Gene: GDB:GNB1
A:Cross-references: GDB:119279; OMIM:139380
A:Map position: 1p36-1p31.2
C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C:Keywords: GTP binding; heterotrimer; signal transduction
F:51-84/Domain: WD repeat homology <WD1>
F:88-126/Domain: WD repeat homology <WD2>
F:139-171/Domain: WD repeat homology <WD3>
F:180-213/Domain: WD repeat homology <WD4>
F:222-255/Domain: WD repeat homology <WD5>
F:263-299/Domain: WD repeat homology <WD6>
F:308-340/Domain: WD repeat homology <WD7>

Query Match 87.2%; Score 1578; DB 1; Length 340;
Best Local Similarity 83.2%; Pred. No. 2.1e-125;
Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAELKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
Db 1 MSELQRLRQEAELKQIADARKACADVTLSQITNNIDPVGRQMRTRRLRGLAKIYA 60
QY 61 MHMATDSKLVASASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGLDNN 120
Db 61 MHMTDSRLVLSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGLDNN 120
QY 121 CSIYNLKSREGNVKVSRELTAHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQOKTVE 180
Db 121 CSIYNLKSREGNVKVSRELTAHTGYLSCRFLLDNNIVTSSGDTTCALMDIETGQOKTVE 180
QY 181 VGHGDCMSLAVSPDENLFIISGACDASAKLMDVREGTCRQFTGHESDINAICFFPNGEA 240
Db 181 TGHGDMVSLSLAPDTRFLVSGACDASAKLMDVREGTCRQFTGHESDINAICFFPNGEA 240
QY 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFLSGLRLLFAGYDDFNWDSM 300
Db 241 FATGSDATCRLFDLRADQELMTYSHDNIIIGITSVSFSKGRLLLAGYDDFNWWDAL 300
QY 301 KSERVGLSGHNDNRVSCIGVTADGMAVATGWSWDSFLKIWN 340
Db 301 KADRAGVLAGHNDNRVSCIGVTDDGMAVATGWSWDSFLKIWN 340

RESULT 4

RGBOB1
GTP-binding regulatory protein beta-1 chain - bovine
N:Alternate names: guanine nucleotide binding protein beta-1 chain; heterotrimeric G-
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C:Accession: A24225; A25457
R:Sugimoto, K.; Nakada, T.; Tanabe, T.; Takahashi, H.; Noda, M.; Minamino, N.; Kangaw
FEBS Lett. 191, 235-240, 1985
A:Title: Primary structure of the beta-subunit of bovine transducin deduced from the
A:Reference number: A24225; MUID:86030675
A:Accession: A24225
A:Molecule type: mRNA
A:Residues: 1-340 <STG>
A:Cross-references: GB:X03073
R:Fong, H.K.W.; Hurley, J.B.; Hopkins, R.S.; Mlake-Lye, R.; Johnson, M.S.; Doolittle,
Proc. Natl. Acad. Sci. U.S.A. 83, 2162-2166, 1986
A:Title: Repetitive segmental structure of the transducin beta subunit: homology with
A:Reference number: A25457; MUID:86177563
A:Accession: A25457
A:Molecule type: mRNA
A:Residues: 1-340 <FON>

A:Cross-references: GB:M13236; NID:g163782; PIDN:AAA30792.1; PID:g163783
 C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
 ains. The beta and gamma chains, required for GTPase activity, appear to be common to al
 rase; it is specific for each type of G protein.
 C:Comment: In mammals, four distinct types of beta chains have been found.
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 C:Keywords: GTP binding; heterotrimer; signal transduction
 F:51-84/Domain: WD repeat homology <WD1>
 F:88-126/Domain: WD repeat homology <WD2>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology <WD7>

Query Match 87.2%; Score 1578; DB 1; Length 340;
 Best Local Similarity 83.2%; Pred. No. 2.1e-125;
 Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGEMQLRQEAQLKKQIADARKACADVTLLAELVSGLEVGRVQMRTRTLRGLAKIYA 60
 1 MSELQRLQEAQLKKQIADARKACADATLSQITNNIDPVGRQMRTRTLRGLAKIYA 60
 QY 61 MHWATDSKLVASASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
 61 MHWGTDSRLVSAQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNYVACGGLDNI 120
 QY 121 CSITNLSKREGNVKVSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQQTTF 180
 121 CSITNLSKREGNVKVSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQQTTF 180
 QY 181 VGHGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCRQFTGHESDINAIICFFPNGEA 240
 181 TGHGDCVMSLAPDTRFLVSGACDASAKLMDVREGTCRQFTGHESDINAIICFFPNGEA 240
 QY 241 ICTGSDASCRLFLRADQELICFSHESITICGITSVAFLSGLRFLFAGYDDFNCNVWDSM 300
 241 FATGSDATCRLFLRADQELIMTYSHDNIICGITSVSFSKSGRLLAGYDDFNCNVWDAL 300
 QY 301 KSERVGLSGHDNRVSCIGVTADGMAVATGWSDFLKIWN 340
 301 KADRAGVLAGHDNRVSCIGVTDDGMAVATGWSDFLKIWN 340

RESULT 5

JC5057
 G protein beta 1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Aug-1999
 C:Accession: JC5057
 R:Qiu, R.; Schimmer, B.P.
 Gene 175, 275-277, 1996
 A:Title: cDNA for the beta 1 subunit of guanyl nucleotide-binding regulatory proteins fr
 A:Reference number: JC5057; MUID:97074684
 A:Accession: JC5057
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-340 <QIU>
 A:Cross-references: GB:U29055; NID:g868168; PIDN:AAC52905.1; PID:g868169
 A:Experimental source: adrenal glands
 C:Comment: This protein is a membrane-associated guanyl nucleotide-binding regulatory he
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:51-84/Domain: WD repeat homology <WD1>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology #status atypical <WD7>

Query Match 87.2%; Score 1578; DB 2; Length 340;
 Best Local Similarity 83.2%; Pred. No. 2.1e-125;

Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGEMQLRQEAQLKKQIADARKACADVTLLAELVSGLEVGRVQMRTRTLRGLAKIYA 60
 1 MSELQRLQEAQLKKQIADARKACADATLSQITNNIDPVGRQMRTRTLRGLAKIYA 60
 QY 61 MHWATDSKLVASASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
 61 MHWGTDSRLVSAQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNYVACGGLDNI 120
 QY 121 CSITNLSKREGNVKVSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQQTTF 180
 121 CSITNLSKREGNVKVSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQQTTF 180
 QY 181 VGHGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCRQFTGHESDINAIICFFPNGEA 240
 181 TGHGDCVMSLAPDTRFLVSGACDASAKLMDVREGTCRQFTGHESDINAIICFFPNGEA 240
 QY 241 ICTGSDASCRLFLRADQELICFSHESITICGITSVAFLSGLRFLFAGYDDFNCNVWDSM 300
 241 FATGSDATCRLFLRADQELIMTYSHDNIICGITSVSFSKSGRLLAGYDDFNCNVWDAL 300
 QY 301 KSERVGLSGHDNRVSCIGVTADGMAVATGWSDFLKIWN 340
 301 KADRAGVLAGHDNRVSCIGVTDDGMAVATGWSDFLKIWN 340

RESULT 6

RGHUB2
 GTP-binding regulatory protein beta-2 chain - human
 N:Alternate names: guanine nucleotide binding protein beta-2 chain; heterotrimeric G-
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: B26617; B28040
 R:Fong, H.K.W.; Amatrua III, T.T.; Birren, B.W.; Simon, M.I.
 Proc. Natl. Acad. Sci. U.S.A. 84, 3792-3796, 1987
 A:Title: Distinct forms of the beta-subunit of GTP-binding regulatory proteins identi
 A:Reference number: A94155; MUID:87231903
 A:Accession: B26617
 A:Molecule type: mRNA
 A:Residues: 1-340 <FON>
 A:Cross-references: GB:M16514; NID:g183469; PIDN:AAA03179.1; PID:g386751
 R:Gao, B.; Gilman, A.G.; Robishaw, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6122-6125, 1987
 A:Title: A second form of the beta subunit of signal-transducing G proteins.
 A:Reference number: A94177; MUID:87317607
 A:Accession: B28040
 A:Molecule type: mRNA
 A:Residues: 1-340 <GAO>
 A:Cross-references: GB:M16538
 C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
 ains. The beta and gamma chains, required for GTPase activity, appear to be common to
 rase; it is specific for each type of G protein.
 C:Comment: In mammals, four distinct types of beta chains have been found.
 C:Genetics:
 A:Gene: GDB:GNB2
 A:Cross-references: GDB:120004; OMIM:139390
 A:Map position: 7q21.3-7q22.1
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:51-84/Domain: WD repeat homology <WD1>
 F:88-126/Domain: WD repeat homology <WD2>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology <WD7>

Query Match 84.5%; Score 1528; DB 1; Length 340;
 Best Local Similarity 80.9%; Pred. No. 3.5e-121;
 Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

```

QY 1 MGEMEQLRQAEQKQIADARKACADVTIAELVSGLEVGRVOMRTRTLRLGHLAKIYA 60
Db 1 MSELQDLROEAQELRNQIDARKACAGDSTLTQITAGLDPVGRIOQRTRTLRLGHLAKIYA 60
QY 61 MHMATDSKLLVASASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
Db 61 MHMGTDSSLVLSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSIYNLKSREGNVKVSRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVE 180
Db 121 CSIYSLKTRREGNVKVSRELPGHTGYLSCCRFLDDNQIITSSGDTTCALWDIETGQOYVGF 180
QY 181 VGHGTDCMSLAVSPDENLFIISGACDASAKLMDVREGTCROTFTGHESDINAIKCFPNGEA 240
Db 181 AGHSGDVMSLADPGRFTVSGACDASIKLMDVDSMCRQFTIGHESDINAVAFPPNGYA 240
QY 241 ICTGSDASCRLFDLRADQELICFSHESIIGITSVAFLSGRLIFAGYDDFNCNVWDSM 300
Db 241 FTTGSDDATCRLFDLRADQELIMYSHDNICGITSVAFSRSGRLILLAGYDDFNCNIMWDM 300
QY 301 KSERVGLSGHDNRVSCIGVTADGMAVATGWSWDFLKIWN 340
Db 301 KGDRAVLGAGHDNRVSCIGVTDDGMAVATGWSWDFLKIWN 340

```

```

RESULT 7
T20830
hypothetical protein F13D12.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T20830
R:Colles, L.
submitted to the EMBL Data Library, April 1995
A:Reference number: Z19330
A:Accession: T20830
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-340 <WIL>
A:Cross-references: EMBL:Z49127; PIDN:CAA88948.1; GSPDB:GN00020; CESP:F13D12.7
A:Experimental source: clone F13D12
C:Genetics:
A:Gene: CESP:F13D12.7
A:Map position: 2
A:Introns: 19/3; 57/3; 89/3; 116/1; 166/2; 209/3; 233/3; 306/1
C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

```

```

Query Match 84.3%; Score 1525; DB 2; Length 340;
Best Local Similarity 81.5%; Pred. No. 6.2e-121;
Matches 277; Conservative 29; Mismatches 34; Indels 0; Gaps 0;

```

```

QY 1 MGEMEQLRQAEQKQIADARKACADVTIAELVSGLEVGRVOMRTRTLRLGHLAKIYA 60
Db 1 MSELQDLROEAQELRNQIDARKACAGDSTLTQITAGLDPVGRIOQRTRTLRLGHLAKIYA 60
QY 61 MHMATDSKLLVASASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
Db 61 MHWASDSRLVLSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSIYNLKSREGNVKVSRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVE 180
Db 121 CSIYSLKTRREGNVKVSRELPGHTGYLSCCRFLDDNQIITSSGDTTCALWDIETGQOCTAF 180
QY 181 VGHGTDCMSLAVSPDENLFIISGACDASAKLMDVREGTCROTFTGHESDINAIKCFPNGEA 240
Db 181 TGHGTGVMSLSLSPDFTFTISGACDASAKLMDIRDMCKQTFPGHESDINAVAFPPSGNA 240
QY 241 ICTGSDASCRLFDLRADQELICFSHESIIGITSVAFLSGRLIFAGYDDFNCNVWDSM 300
Db 241 FATGSDATCRLFDLRADQELIMYSHDNICGITSVAFSRSGRLILLAGYDDFNCNIMWDM 300
QY 301 KSERVGLSGHDNRVSCIGVTADGMAVATGWSWDFLKIWN 340
Db 301 KSERVGLSGHDNRVSCIGVTADGMAVATGWSWDFLKIWN 340

```

```

Db 301 RQERAGVLGAGHDNRVSCIGVTEDGMAVCTGWSWDFLKIWN 340

```

```

RESULT 8
RGKWB
GTP-binding regulatory protein beta chain - Caenorhabditis elegans
N:Alternate names: guanine nucleotide binding protein beta chain; heterotrimeric G-pr
C:Species: Caenorhabditis elegans
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C:Accession: S09591
R:van der Voorn, L.; Gebbink, M.; Plasterk, R.H.A.; Ploegh, H.L.
J. Mol. Biol. 213, 17-26, 1990
A:Title: Characterization of a G-protein beta-subunit gene from the nematode Caenorha
A:Reference number: S09591; MUID:90250769
A:Accession: S09591
A:Molecule type: DNA
A:Residues: 1-340 <VAN>
A:Cross-references: EMBL:X17497; NID:96642; PIDN:CAA35532.1; PID:96643
C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
ains. The beta and gamma chains, required for GTPase activity, appear to be common to
rase; it is specific for each type of G protein.
C:Comment: In mammals, four distinct types of beta chains have been found.
C:Genetics:
A:Introns: 19/3; 57/3; 89/3; 115/2; 166/1; 209/3; 233/3; 305/2
C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
C:Keywords: GTP binding; heterotrimer; signal transduction
F:51-84/Domain: WD repeat homology <WD1>
F:88-126/Domain: WD repeat homology <WD2>
F:139-171/Domain: WD repeat homology <WD3>
F:180-213/Domain: WD repeat homology <WD4>
F:222-255/Domain: WD repeat homology <WD5>
F:263-299/Domain: WD repeat homology <WD6>
F:308-340/Domain: WD repeat homology <WD7>

```

```

Query Match 84.0%; Score 1520; DB 1; Length 340;
Best Local Similarity 81.2%; Pred. No. 1.6e-120;
Matches 276; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

```

```

QY 1 MGEMEQLRQAEQKQIADARKACADVTIAELVSGLEVGRVOMRTRTLRLGHLAKIYA 60
Db 1 MSELQDLROEAQELRNQIDARKACAGDSTLTQITAGLDPVGRIOQRTRTLRLGHLAKIYA 60
QY 61 MHMATDSKLLVASASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
Db 61 MHWASDSRLVLSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 120
QY 121 CSIYNLKSREGNVKVSRELTAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVE 180
Db 121 CSIYSLKTRREGNVKVSRELPGHTGYLSCCRFLDDNQIITSSGDTTCALWDIETGQOCTAF 180
QY 181 VGHGTDCMSLAVSPDENLFIISGACDASAKLMDVREGTCROTFTGHESDINAIKCFPNGEA 240
Db 181 TGHGTGVMSLSLSPDFTFTISGACDASAKLMDIRDMCKQTFPGHESDINAVAFPPSGNR 240
QY 241 ICTGSDASCRLFDLRADQELICFSHESIIGITSVAFLSGRLIFAGYDDFNCNVWDSM 300
Db 241 FATGSDATCRLFDLRADQELIMYSHDNICGITSVAFSRSGRLILLAGYDDFNCNIMWDM 300
QY 301 KSERVGLSGHDNRVSCIGVTADGMAVATGWSWDFLKIWN 340
Db 301 RQERAGVLGAGHDNRVSCIGVTEDGMAVCTGWSWDFLKIWN 340

```

```

RESULT 9
RGMSB4
GTP-binding regulatory protein beta-4 chain - mouse
N:Alternate names: guanine nucleotide binding protein beta-4 chain; heterotrimeric G-
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C:Accession: J50669
R: von Weizsaecker, E.; Strathmann, M.P.; Simon, M.I.
Biochem. Biophys. Res. Commun. 183, 350-356, 1992

```

A:Title: Diversity among the beta subunits of heterotrimeric GTP-binding proteins: chara
A:Reference number: JS0669; MUID:92181467
A:Accession: JS0669

A:Molecule type: mRNA
A:Residues: 1-340 <VON>

A:Cross-references: GB:S6124; NID:g246469; PIDN:AB21609.1; PID:g246470
C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
ains. The beta and gamma chains, required for GTPase activity, appear to be common to all
rase; it is specific for each type of G protein.

C:Comment: In mammals, four distinct types of beta chains have been found.

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C:Keywords: GTP binding; heterotrimer; signal transduction

F:51-84/Domain: WD repeat homology <WD1>

F:88-126/Domain: WD repeat homology <WD2>

F:139-171/Domain: WD repeat homology <WD3>

F:180-213/Domain: WD repeat homology <WD4>

F:222-255/Domain: WD repeat homology <WD5>

F:263-299/Domain: WD repeat homology <WD6>

F:308-340/Domain: WD repeat homology <WD7>

Query Match 82.9%; Score 1500; DB 1; Length 340;

Best Local Similarity 78.8%; Pred. No. 8e-119;

Matches 268; Conservative 38; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGEMEQLRQAEQQLKQIADARKACADVTLLAEVSGLEVGRVQMRTRLRGLAKIYA 60

Db 1 MSELQRLQAEQRLNQIQDARKACNDATLVQITSNMDVGRIGMRTKRLRGLAKIYA 60

QY 61 MHMATDSKLVSASQDGKLIWDSYTNKVAIPLRSSWMTCAVAPSGNFVACGLDNM 120

Db 61 MHMGYDSRLVSAQDGKLIWDSYTNKVAIPLRSSWMTCAVAPSGNFVACGLDNI 120

QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQKTVE 180

Db 121 CSIYNLKTREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQKTTF 180

QY 181 VGHGTDCMSLAVSPDFNLFISGACDASAKLMDVREGTCRQFTGHESDINAIKCFPNGEA 240

Db 181 TGHSGDVMSLSPDLKTFVSGACDASSKLMDIRDMCRQSFTHISIDINAVSFPPSGYA 240

QY 241 ICTGSDASCRLFLRADQELICFSHESIIGTITSVAFSLSGRLLFAGYDDENCNVWDSM 300

Db 241 FATGSDATCRLFLRADQELIYSHDNIIGTITSVAFSKSGRLLAGYDDENCVWDAL 300

QY 301 KSERVGLSGHDNRVSCLGVTADGMAVATGWSDFLKIWN 340

Db 301 KGRSGVLAGHDNRVSCLGVTDDGMAVATGWSDFLKIWN 340

RESULT 10

S34348 GTP-binding regulatory protein beta chain - great pond snail

N:Alternate names: guanine nucleotide regulatory protein beta chain

C:Species: Lymnaea stagnalis (great pond snail)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999

C:Accession: S69891; S34348

R:Knol, J.C.; Roovers, E.; van Kesteren, E.R.; Planta, R.J.; Vreugdenhil, E.; van Heerik

Biochim. Biophys. Acta 1222, 129-133, 1994

A:Title: A G-protein beta subunit that is expressed in the central nervous system of the

A:Reference number: S69891; MUID:94242793

A:Accession: S69891

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-341 <KN2>

A:Cross-references: EMBL:Z23105; NID:g312631; PIDN:CAA80652.1; PID:g312632

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

F:52-85/Domain: WD repeat homology <WD1>

F:181-214/Domain: WD repeat homology <WD4>

F:267-300/Domain: WD repeat homology <WD6>

F:309-341/Domain: WD repeat homology #status atypical <WD7>

Query Match 81.8%; Score 1480; DB 2; Length 341;
Best Local Similarity 79.6%; Pred. No. 3.9e-117;
Matches 269; Conservative 30; Mismatches 39; Indels 0; Gaps 0;

QY 3 EMEQLRQAEQQLKQIADARKACADVTLLAEVSGLEVGRVQMRTRLRGLAKIYAMH 62

Db 4 DLEALRQETQQLKQIADARKACADVTLLAEVSGLEVGRVQMRTRLRGLAKIYAMH 63

QY 63 WATDSKLVSASQDGKLIWDSYTNKVAIPLRSSWMTCAVAPSGNFVACGLDNMCS 122

Db 64 WASDSRLVSAQDGKLIWDSYTNKVAIPLRSSWMTCAVAPSGNFVACGLDNICS 123

QY 123 IYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQKTVE 182

Db 124 IYSLKTREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQKTVE 183

QY 183 HTGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCRQFTGHESDINAIKCFPNGEA 242

Db 184 HTGDVMSLSPDLKTFVSGACDASAKLMDVREGTCRQFTGHESDINAIKCFPNGEA 243

QY 243 TGSDDASCRLFLRADQELICFSHESIIGTITSVAFSLSGRLLFAGYDDENCNVWDSMKS 302

Db 244 TGSDDATCRLFLRADQELIYSHDNIIGTITSVAFSKSGRLLAGYDDENCNVWDVLKQ 303

QY 303 ERYGILSGHDNRVSCLGVTADGMAVATGWSDFLKIWN 340

Db 304 EYHGVLAGHDNRVSCLGVTEDGSAVATGWSDFLKIWN 341

RESULT 11

RGBOB2 GTP-binding regulatory protein beta-2 chain - bovine (fragment)

N:Alternate names: guanine nucleotide binding protein beta-2 chain; heterotrimeric G-

C:Species: Bos primigenius taurus (cattle)

C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C:Accession: A26617; A28040

R:Fong, H.K.W.; Amatruda III, T.T.; Birren, B.W.; Simon, M.I.

Proc. Natl. Acad. Sci. U.S.A. 84, 3792-3796, 1987

A:Title: Distinct forms of the beta-subunit of GTP-binding regulatory proteins identl

A:Reference number: A94155; MUID:87231903

A:Accession: A26617

A:Molecule type: mRNA

A:Residues: 1-326 <FON>

A:Cross-references: GB:M16480; NID:g163112; PIDN:AAA30553.1; PID:g163113

R:Gao, B.; Gilman, A.G.; Robishaw, J.D.

Proc. Natl. Acad. Sci. U.S.A. 84, 6122-6125, 1987

A:Title: A second form of the beta subunit of signal-transducing G proteins.

A:Reference number: A94177; MUID:87317607

A:Accession: A28040

A:Molecule type: mRNA

A:Residues: 88-270, 'V', 272-302 <GAO>

A:Cross-references: GB:M16539; NID:g163110; PIDN:AAA30552.1; PID:g163111

C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re

ains. The beta and gamma chains, required for GTPase activity, appear to be common to

rase; it is specific for each type of G protein.

C:Comment: In mammals, four distinct types of beta chains have been found.

C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology

C:Keywords: GTP binding; heterotrimer; signal transduction

F:37-70/Domain: WD repeat homology <WD1>

F:74-112/Domain: WD repeat homology <WD2>

F:125-157/Domain: WD repeat homology <WD3>

F:166-199/Domain: WD repeat homology <WD4>

F:208-241/Domain: WD repeat homology <WD5>

F:249-285/Domain: WD repeat homology <WD6>

F:294-326/Domain: WD repeat homology <WD7>

Query Match 81.2%; Score 1469; DB 1; Length 326;

Best Local Similarity 80.7%; Pred. No. 3.1e-116;

Matches 263; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 15 KQIADARKACADVTLLAEVSGLEVGRVQMRTRLRGLAKIYAMHWATDSKLVSAS 74

Db 15 KQIADARKACADVTLLAEVSGLEVGRVQMRTRLRGLAKIYAMHWATDSKLVSAS 74

Db 1 RNOIRDARKACGDSLTQITAGLDPVGRIOQMTTRTLRGLAKIYAMHMGTDRLVSAS 60
 QY 75 QDGLIWMDSYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNMCSITYNLKSREGNVK 134
 Db 61 QDGLIWMDSYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNMCSITYNLKSREGNVK 120
 QY 135 VSRELSTHTGYSRFLDNNIVTSSGDTTCALWDIETGQOKTVFVGHGTGDCMSLAVSP 194
 Db 121 VSRELSTHTGYSRFLDNNIVTSSGDTTCALWDIETGQOKTVFVGHGTGDCMSLAVSP 180
 QY 195 DFNLFISGACDASAKLMDVREGTCRQFTGHESDINAICTGSDDASCRLFD 254
 Db 181 DGRFVSGACDASIKLMDVDSMCRQFTGHESDINAVAFPPNGYFTTGSDDATCRLFD 240
 QY 255 LRADQELICFSHESITIGTSVAFSLSGRLLFAGYDDFNCSNVWDSKSERVGLSGHDNR 314
 Db 241 LRADQELIWMYSHDNICGITSVAFSRSRGLLAGYDDFNCSNVWDSKSERVGLSGHDNR 300
 QY 315 VSCIGVTADGMAVATGWSWDFLKIWN 340
 Db 301 VSCIGVTDDGMAVATGWSWDFLKIWN 326

RESULT 12

RGOOBE

GTP-binding regulatory protein beta chain - northern European squid

N:Alternate names: guanine nucleotide binding protein beta chain; heterotrimeric G-protein
 C:Species: Loligo forbesi (northern European squid)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: S13302

R:Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Findlay, J.B.C.
 Biochem. J. 273, 225-228, 1991
 A:Title: Sequence of the beta-subunit of the phosphatidylinositol-specific phospholipase
 A:Reference number: S13302; MUID:91113146
 A:Accession: S13302

A:Molecule type: mRNA
 A:Residues: 1-341 <RYB>
 A:Cross-references: EMBL:X56757; NID:99507; PIDN:CAA40077.1; PID:99508

C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
 ains. The beta and gamma chains, required for GTPase activity, appear to be common to all
 rase; it is specific for each type of G protein.
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 C:Keywords: GTP binding; heterotrimer; signal transduction
 F:52-85/Domain: WD repeat homology <WD1>
 F:89-127/Domain: WD repeat homology <WD2>
 F:140-172/Domain: WD repeat homology <WD3>
 F:181-214/Domain: WD repeat homology <WD4>
 F:223-256/Domain: WD repeat homology <WD5>
 F:264-300/Domain: WD repeat homology <WD6>
 F:309-341/Domain: WD repeat homology <WD7>

Query Match 80.98; Score 1463; DB 1; Length 341;
 Best Local Similarity 79.0%; Pred. No. 1e-115;
 Matches 267; Conservative 32; Mismatches 39; Indels 0; Gaps 0;

QY 3 EMEQLRQEAQKQIADARKACADVTIAELVSGLEVGRVQMTTRTLRGLAKIYAMH 62
 Db 4 EELALRQETQKQIADARKACADVTIAELVSGLEVGRVQMTTRTLRGLAKIYAMH 63
 QY 63 WATDSKLLVSASQDGLIWMDSYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNMCS 122
 Db 64 WASDSRLVVSASQDGLIWMDSYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNMCS 123
 QY 123 IYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQOKTVFV 182
 Db 124 IYSLKTRREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQOKTVFV 183
 QY 183 HTGDCMSLAVSPDNLFISGACDASAKLMDVREGTCRQFTGHESDINAICTGSDDASCRLFD 242
 Db 184 HTGDMVSLSLAPDMRFTVSGACDASAKLMDVREGTCRQFTGHESDINAICTGSDDASCRLFD 243
 QY 243 TGSDDASCRLFDLRADQELICFSHESITIGTSVAFSLSGRLLFAGYDDFNCSNVWDSKMS 302

Db 244 TGSDDASCRLFDLRADQELICFSHESITIGTSVAFSLSGRLLFAGYDDFNCSNVWDSKMS 303
 QY 303 ERVGLSGHDNRVSCIGVTADGMAVATGWSWDFLKIWN 340
 Db 304 ERAGVLAGHDNRVSCIGVTEDGMAVATGWSWDFLKIWN 341

RESULT 13

RGFBH

GTP-binding regulatory protein beta chain homolog - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
 C:Accession: A40489

R:Yaritz, S.; Provost, N.M.; Hurley, J.B.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7134-7138, 1988
 A:Title: Cloning of a Drosophila melanogaster guanine nucleotide regulatory protein b
 A:Reference number: A40489; MUID:89017152
 A:Accession: A40489

A:Molecule type: mRNA
 A:Residues: 1-340 <YAR>
 A:Cross-references: GB:M22567; GB:J04083; NID:9157497; PIDN:AAB59247.1; PID:9157498

C:Genetics:
 A:Gene: FlyBase:G&bgtr
 A:Cross-references: FlyBase:FBgn0001105

A:Map position: X13F
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:51-84/Domain: WD repeat homology <WD1>
 F:88-126/Domain: WD repeat homology <WD2>
 F:139-171/Domain: WD repeat homology <WD3>
 F:180-213/Domain: WD repeat homology <WD4>
 F:222-255/Domain: WD repeat homology <WD5>
 F:263-299/Domain: WD repeat homology <WD6>
 F:308-340/Domain: WD repeat homology <WD7>

Query Match 80.7%; Score 1459; DB 1; Length 340;
 Best Local Similarity 77.4%; Pred. No. 2.3e-115;
 Matches 263; Conservative 35; Mismatches 42; Indels 0; Gaps 0;

QY 1 MGEMLRQEAQKQIADARKACADVTIAELVSGLEVGRVQMTTRTLRGLAKIY 60
 Db 1 MNELDSLQEAESLKNAIADARKACADVTIAELVSGLEVGRVQMTTRTLRGLAKIY 60
 QY 61 MHWATDSKLLVSASQDGLIWMDSYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 Db 61 MHWGNDRLVVSASQDGLIWMDSYTNKVAIPLRSSWMTCAVAPSGNFVACGGIDNM 120
 QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQOKTVF 180
 Db 121 CSIYNLKTREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDMSCGLWDIETGLQVTSF 180
 QY 181 VGHGTDCMSLAVSPDNLFISGACDASAKLMDVREGTCRQFTGHESDINAICTGSDDASCRLFD 240
 Db 181 LGHTGDVMSLAPDQCKTFVSGACDASAKLMDIREGVCKQFTFGHESDINAVTFPPNGQA 240
 QY 241 ICTGSDDASCRLFDLRADQELICFSHESITIGTSVAFSLSGRLLFAGYDDFNCSNVWDSM 300
 Db 241 FATGSDDATCRLFDLRADQELIWMYSHDNIIICGITSVAFSRSRGLLAGYDDFNCSNVWDTM 300
 QY 301 KSERVGLSGHDNRVSCIGVTADGMAVATGWSWDFLKIWN 340
 Db 301 KAERSGILAGHDNRVSCIGVTENGMAVATGWSWDFLKIWN 340

RESULT 14

A47370

GTP-binding regulatory protein beta chain - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum
 C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
 C:Accession: A47370

R:Lilly, P.; Wu, L.; Welker, D.L.; Devreotes, P.N.
 Genes Dev. 7, 986-995, 1993

A:Title: A G-protein beta-subunit is essential for Dictyostelium development.
 A:Reference number: A47370; MUID:93279474
 A:Accession: A47370
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-347 <LIL>
 A:Cross-references: GB:X73641; NID:9460980; PIDN:CA52018.1; PID:9460981
 A:Note: sequence extracted from NCBI backbone (NCBIN:132987, NCBIN:132989, NCBIN:132991,
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:146-178/Domain: WD repeat homology <WD2>
 F:187-220/Domain: WD repeat homology <WD3>
 F:273-306/Domain: WD repeat homology <WD5>
 F:315-347/Domain: WD repeat homology #status atypical <WD6>

Query Match 68.4%; Score 1238; DB 2; Length 347;
 Best Local Similarity 66.7%; Pred. No. 9.6e-97;
 Matches 226; Conservative 47; Mismatches 64; Indels 2; Gaps 1;
 QY 3 EMEQLROEAQLKQIADARKACADVTTLAEVSGLEVGRVQ--MRTRTLGHAKIYA 60
 Db 8 KIQARDAESMEKEQIRANRDVMDTTLKFTTRDLPGLPKMEKIKVRNLKGHLAKIYA 67
 QY 61 MHMATDSKLIVASQDGLIWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 Db 68 MHMAEDNVHLVSAQDGLIWDGLTTLNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNI 127
 QY 121 CSIYNLKSREGNVKVSRELSTHTGYLSCCRFLDNNIIVTSSGDTTCALWDIETGQKTVF 180
 Db 128 CSIYNLKSREGPIRVCRELNSTHTGYLSCCRFLDNRQIVTSSGDMTCILMDVENGTITEF 187
 QY 181 VGHGTGDCMSLAVSPDENLFIGACDASAKLMDVREGTCRQTFTGHESDINAICFPNGEA 240
 Db 188 SDHNGDVMSVSPDKNYFISGACDATALMDLRSGKCVQFTGHEADINAVQYFPNGLS 247
 QY 241 ICTGSDASCRLFDLRADQELICFSHESIICGITSVAFLSGLRLLFAGYDDFNCNWDSM 300
 Db 248 FGTGSDASCRLFDLRADRELQYTHDNLICGITSVGFSESGRFLFAGYDDFTCNWMDTL 307
 QY 301 KSERVGLISGHNDNRVSCIGVTADGMAVATGSDWDFLKIW 339
 Db 308 KGERVLSLTGHGNRVSCIGVPTDGMALCTGSDWDFLKIW 346

RESULT 15
 A54969
 beta-5 GTP-binding protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 13-Aug-1999
 C:Accession: A54969
 R:Watson, A.J.; Katz, A.; Simon, M.L.
 J. Biol. Chem. 269, 22150-22156, 1994
 A:Title: A fifth member of the mammalian G-protein beta-subunit family. Expression in br
 A:Reference number: A54969; MUID:94350964
 A:Accession: A54969
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-353 <WAT>
 A:Cross-references: GB:L34290; NID:91237255; PIDN:AAA93084.1; PID:9557738
 C:Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology
 F:59-92/Domain: WD repeat homology <WD1>
 F:149-182/Domain: WD repeat homology <WD3>
 F:193-226/Domain: WD repeat homology <WD4>
 F:279-312/Domain: WD repeat homology <WD6>
 F:321-353/Domain: WD repeat homology #status atypical <WD7>

Query Match 52.4%; Score 948.5; DB 2; Length 353;
 Best Local Similarity 51.9%; Pred. No. 2.4e-72;
 Matches 177; Conservative 57; Mismatches 102; Indels 5; Gaps 3;
 QY 4 MEOLROEAQLKQIADARKACADVTTLAEVSGLEVGRVQMTRTLGHAKIYAMHW 63
 : | : | | | | : : : | | | : : : | : | | | | : | : |

Db 12 LASLKEAESLKGKLEERAKLHDELHQAVEREALGQFVMKTRRTLKGHNKYLQMDW 71
 QY 64 ATDSKLIVASQDGLIWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNMCSI 123
 Db 72 CKDKRRIVSSQDGLIWDSTYTNKEHAWTMCWMACAVAPSGCAIACGGLDNMCSV 131
 QY 124 YNL--KSREGNVKVSRELSTHTGYLSCCRFLD--DNNIIVTSSGDTTCALWDIETGQKTVF 180
 Db 132 YPLTFDKNENMAAKKSVAMHTNYLSACSFITNSDMQILTASGDTTCALWDVESGQLQSF 191
 QY 181 VGHGTGDC--CMSLAVSPDENLFIGACDASAKLMDVREGTCRQTFTGHESDINAICFPNG 238
 Db 192 HGHGADVLCIDLPSETNTFVSGGCKKAMVMDMRSGQCVQAFETHESDVNSVRYPSG 251
 QY 239 EAITGSDASCRLFDLRADQELICFSHESIICGITSVAFLSGLRLLFAGYDDFNCNWMD 298
 Db 252 DAFASGSDATCRLYDLRADREVALYSKESIIFGASSVDFSLSGRLLFAGYNDYTYINWMD 311
 QY 299 SMKSERVGLISGHNDNRVSCIGVTADGMAVATGSDWDFLKIW 339
 Db 312 VLKGSRVSLIFGHENRVSLRVSPDGTAFCSGSDWDFLKIW 352

Search completed: September 28, 2001, 10:33:21
 Job time: 272 sec

Fri Sep 28 10:45:14 2001

us-09-492-029-5.rpt

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:34:28 ; Search time 16.71 Seconds
(without alignments)
697.000 Million cell updates/sec

Title: US-09-492-029-5
Perfect score: 1809
Sequence: 1 MGEMEQLRQAEQLKKQIAD.....TADGMAVATGWSDFLKIMN 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1809	100.0	340	1	GBB3_HUMAN P16520 homo sapien
2	1763	97.5	340	1	GBB3_MOUSE Q61011 mus musculu
3	1762	97.4	340	1	GBB3_RAT P52287 rattus norv
4	1759	97.2	340	1	GBB3_CANFA P79147 canis famil
5	1578	87.2	340	1	GBB1_HUMAN P04901 homo sapien
6	1573	87.0	340	1	GBB1_XENLA P79959 xenopus lae
7	1572	86.9	340	1	GBB1_RAT P54311 rattus norv
8	1528	84.5	340	1	GBB2_MOUSE P11016 homo sapien
9	1521	84.1	340	1	GBB2_MOUSE P54312 mus musculu
10	1520	84.0	340	1	GBB1_CAEL P17343 caenorhabdi
11	1500	82.9	340	1	GBB2_RAT P54313 rattus norv
12	1500	82.9	340	1	GBB4_MOUSE P29387 mus musculu
13	1480	81.8	341	1	GBB_LYMST Q08706 lymnaea sta
14	1479	81.8	340	1	GBB1_HOMAM O45040 homarus ame
15	1469	81.2	326	1	GBB2_BOVIN P11017 bos taurus
16	1463	80.9	341	1	GBB1_LOLEO P23232 loligo forb
17	1459	80.7	340	1	GBB1_DROME P26308 drosophila
18	1438	68.4	347	1	GBB_DICDI P36408 dictyosteli
19	1198	66.2	359	1	GBB_CRYPA O14435 cryphonectr
20	949.5	52.5	353	1	GBB5_HUMAN O14775 homo sapien
21	948.5	52.4	356	1	GBB5_MOUSE P54314 mus musculu
22	927.5	51.3	356	1	GBB5_CAEL Q20636 caenorhabdi
23	847	46.8	380	1	GBB_ORYSA Q40687 oryza sativ
24	831	45.9	380	1	GBB_MAIZE P49178 zea mays (m
25	824	45.6	377	1	GBB1_TOBAC P93397 nicotiana t
26	822	45.4	375	1	GBB3_TOBAC Q40507 nicotiana t
27	822	45.4	377	1	GBB2_TOBAC P93398 nicotiana t
28	822	45.4	377	1	GBB_SOLTU P93563 solanum tub
29	815	45.1	377	1	GBB_ARATH P49177 arabidopsis
30	808	44.7	377	1	GBB2_DROME P29829 drosophila
31	790	43.7	377	1	GBB_NICPL P93339 nicotiana p
32	668	36.9	305	1	GBB_SCHPO O10282 schizosacch
33	647	35.8	423	1	GBB_YEAST P18851 saccharomyc

34	377.5	20.9	1356	1	HET1_PODAN	Q00808 podospora a
35	343	19.0	742	1	PKWA_THECU	P49695 thermomonos
36	308.5	17.1	465	1	PR04_YEAST	P20053 saccharomyc
37	307.5	17.0	317	1	GBLP_BRARE	O42248 brachydanio
38	305.5	16.9	317	1	GBLP_HUMAN	P25388 homo sapien
39	304	16.8	361	1	WDS_DROME	Q9V3J8 drosophila
40	302.5	16.7	316	1	GBLP_BIOGL	Q93134 biomphalari
41	299.5	16.6	317	1	GBLP_ORENI	O42249 oreochromis
42	299.5	16.6	318	1	GBLP_TRYBB	Q94775 trypanosoma
43	299.5	16.6	1693	1	Y163_SYNY3	Q55563 synchocyst
44	297	16.4	554	1	PR04_ARATH	O22212 arabidopsis
45	296	16.4	704	1	T2D4_DROME	P49846 drosophila

ALIGNMENTS

RESULT 1
GBB3_HUMAN
ID GBB3_HUMAN STANDARD: PRT; 340 AA.
AC P16520;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3
DE (TRANSDUCIN BETA CHAIN 3).
GN GNB3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90192801; PubMed=2107550;
RA Levine M.A., Smallwood P.M., Moen P.T. Jr., Helman L.J., Ahn T.G.;
RT "Molecular cloning of beta 3 subunit, a third form of the G protein
beta-subunit polypeptide."
RT Proc. Natl. Acad. Sci. U.S.A. 87:2329-2333(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96303695; PubMed=8723724;
RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E.,
RA Spanos S., Mailey T., Gibbs R.A.;
RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
genes at human chromosome 12p13."
RL Genome Res. 6:314-326(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Busch S., Dyhr W., Siefert W.;
Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
EFFECTOR INTERACTION.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL: M31328; AAAS2582.1; -
CC EMBL: U47924; AAB51313.1; -
CC EMBL: Y12050; CAA72779.1; -
CC EMBL: Y12051; CAA72779.1; JOINED.
CC EMBL: Y12052; CAA72779.1; JOINED.
CC EMBL: Y12053; CAA72779.1; JOINED.
CC EMBL: Y12054; CAA72779.1; JOINED.

DR EMBL; Y12055; CAA72779.1; JOINED.
 DR EMBL; Y12056; CAA72779.1; JOINED.
 DR EMBL; Y12057; CAA72779.1; JOINED.
 DR EMBL; Y12058; CAA72779.1; JOINED.
 DR EMBL; Y12059; CAA72779.1; JOINED.
 DR PIR; A35096; RGHUB3.
 DR HSSP; P04901; ITBG.
 DR MIM; 139130; -.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 5.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37221 MW; 896E706A61B8D74F CRC64;

Query Match 100.0%; Score 1809; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 1.5e-152;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGEMEQLRQAEQLKKOIAADARKACADVTLAELVSGLEVGVQMRTRRTLRLGHLAKIYA 60
 DB 1 MGEMEQLRQAEQLKKOIAADARKACADVTLAELVSGLEVGVQMRTRRTLRLGHLAKIYA 60
 QY 61 MHWATDSKLLVSASQDGLIWMDSYTTNKVHAIPLRSSWMTCAYPASGNFVACGGLDNM 120
 DB 61 MHWATDSKLLVSASQDGLIWMDSYTTNKVHAIPLRSSWMTCAYPASGNFVACGGLDNM 120
 QY 121 CSTYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQKTYF 180
 DB 121 CSTYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQKTYF 180
 QY 181 VGHGDCMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTGTHESDINAICFPNGEA 240
 DB 181 VGHGDCMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTGTHESDINAICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELICFSHESIIGITSVAFLSGLRLLFAGYDDFNCNVWDSM 300
 DB 241 ICTGSDASCRLFDLRADQELICFSHESIIGITSVAFLSGLRLLFAGYDDFNCNVWDSM 300
 QY 301 KSERVGIISGHNDNRVSCLGVTADGMAVATGSWDSFLKIWN 340
 DB 301 KSERVGIISGHNDNRVSCLGVTADGMAVATGSWDSFLKIWN 340

RESULT 2
 GBB3_MOUSE
 ID GBB3_MOUSE STANDARD; PRT; 340 AA.
 AC Q61011;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3
 DE (TRANSDUCIN BETA CHAIN 3).
 GN GNB3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,

RA Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W.,
 RA Gibbs R.A.;
 RA Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 199-301 FROM N.A.
 RC STRAIN-CF-1 / HARLAN; TISSUE-Retina;
 RX MEDLINE=97011591; PubMed=8858601;
 RA Williams C.J., Schultz R.M., Kopf G.S.;
 RT "G protein gene expression during mouse oocyte growth and maturation,
 RT and preimplantation embryo development.";
 RL Mol. Reprod. Dev. 44:315-323(1996).
 CC -I- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -I- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -I- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AC002397; AAC36013.1; -.
 DR EMBL; U38494; AAB01725.1; -.
 DR HSSP; P04901; 1GP2.
 DR MGD; MGI:95785; Gnb3.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 2.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 5.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37240 MW; 44BA0F8C0FEDEEB1 CRC64;

Query Match 97.5%; Score 1763; DB 1; Length 340;
 Best Local Similarity 97.1%; Pred. No. 1.7e-148;
 Matches 330; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGEMEQLRQAEQLKKOIAADARKACADVTLAELVSGLEVGVQMRTRRTLRLGHLAKIYA 60
 DB 1 MGEMEQLRQAEQLKKOIAADARKACADVTLAELVSGLEVGVQMRTRRTLRLGHLAKIYA 60
 QY 61 MHWATDSKLLVSASQDGLIWMDSYTTNKVHAIPLRSSWMTCAYPASGNFVACGGLDNM 120
 DB 61 MHWATDSKLLVSASQDGLIWMDSYTTNKVHAIPLRSSWMTCAYPASGNFVACGGLDNM 120
 QY 121 CSTYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQKTYF 180
 DB 121 CSTYNLKSREGNVKVSRELSAHTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQKTYF 180
 QY 181 VGHGDCMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTGTHESDINAICFPNGEA 240
 DB 181 VGHGDCMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTGTHESDINAICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELICFSHESIIGITSVAFLSGLRLLFAGYDDFNCNVWDSM 300
 DB 241 ICTGSDASCRLFDLRADQELICFSHESIIGITSVAFLSGLRLLFAGYDDFNCNVWDSM 300

QY 301 KSERVGLSGHDNRVSCLGVTADGMNAVATGSWDSFLKIWN 340
 Db 301 KSERVGLSGHDNRVSCLGVTADGMNAVATGSWDSFLKIWN 340

RESULT 3

GBB3_RAT STANDARD; PRT; 340 AA.
 ID GBB3_RAT
 AC P52287;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3
 (TRANSDUCIN BETA CHAIN 3).
 GN GNB3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Heart;
 RX MEDLINE=95047499; PubMed=7959013;
 RA Ray K., Robishaw J.D.;
 RT "Cloning and sequencing of a rat heart cDNA encoding a G-protein beta
 subunit related to the human retinal beta 3 subunit."
 RL Gene 149:337-340(1994).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT A HIGH LEVEL IN THE HEART AND AT
 CC A MUCH LOWER LEVEL IN THE BRAIN.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; L29090; AAA62620.1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 5.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37180 MW; 020A41F754E4B1DA CRC64;

Query Match 97.4%; Score 1762; DB 1; Length 340;
 Best Local Similarity 96.5%; Pred. No. 2.1e-148;
 Matches 328; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGEMEQLKQAEQLKKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 MGEMEQLKQAEQLKKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
 QY 61 MHWATDSKLVASASQDGLIYWDSTYTNKVHAIPLRSSWMTCAYPASGNFVACGLDM 120
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 MHWATDSKLVASASQDGLIYWDSTYTNKVHAIPLRSSWMTCAYPASGNFVACGLDM 120
 QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQOKTVE 180
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQOKTVE 180
 QY 181 VGHGTDCMSLAVSPDFNLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 181 VGHGTDCMSLAVSPDYKFLFISGACDASAKLMDVREGTCROTFTGHESDINAICTFPNGEA 240
 QY 241 ICTGSDDASCRLFDLRADQELICFSHESIICGITSVAFSLSGRLLFAGYDDFNCAVWDSM 300
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 241 ICTGSDDASCRLFDLRADQELTAVSHESIICGITSVAFSLSGRLLFAGYDDFNCAVWDSL 300
 QY 301 KSERVGLSGHDNRVSCLGVTADGMNAVATGSWDSFLKIWN 340
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 301 KSERVGLSGHDNRVSCLGVTADGMNAVATGSWDSFLKIWN 340

RESULT 4

GBB3_CANFA STANDARD; PRT; 340 AA.
 ID GBB3_CANFA
 AC P79147;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 3
 (TRANSDUCIN BETA CHAIN 3).
 GN GNB3.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALASKAN MALAMUTE; TISSUE=Retina;
 RX MEDLINE=97409956; PubMed=9266671;
 RA Akhmedov N.B., Piriev N.I., Ray K., Acland G.M., Aguirre G.D.,
 RA Farber D.B.;
 RT "Structure and analysis of the transducin beta3-subunit gene, a
 candidate for inherited cone degeneration (cd) in the dog."
 RL Gene 194:47-56(1997).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; U52916; AAC48760.1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 5.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.

```

FT REPEAT 53 83 WD 1.
FT REPEAT 95 125 WD 2.
FT REPEAT 141 170 WD 3.
FT REPEAT 182 212 WD 4.
FT REPEAT 224 254 WD 5.
FT REPEAT 268 298 WD 6.
FT REPEAT 310 340 WD 7.
SQ SEQUENCE 340 AA; 37144 MW; 8E3B5A5238E29C37 CRC64;

Query Match 97.2%; Score 1759; DB 1; Length 340;
Best Local Similarity 96.8%; Pred. No. 3.9e-148;
Matches 329; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGEMQLROEAELKQIADARKACADVTLLAELVSGLEVGRVQMRTRTLRGLAKIYA 60
Db 1 MGEMQLROEAELKQIADARKACADVTLLAELVSGLEVGRVQMRTRTLRGLAKIYA 60
QY 61 MHWATDSKLVASASQDGLIWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGLDNM 120
Db 61 MHWATDSKLVASASQDGLIWDSTYTNKVHAIPLRSSWMTCAVAPSGNFVACGLDNM 120
QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCRFLLDNNIVTSSGDTFCALMDIETGOQKTVF 180
Db 121 CSIYNLKSREGNVKVSRELSAHTGYLSCRFLLDNNIVTSSGDTFCALMDIETGOQKTVF 180
QY 181 VGHGDCMSLAVSPDENLFIGACDASAKLMDVREGTCRQTFGHSDDINAIKCFPNGEA 240
Db 181 VGHGDCMSLAVSPDENLFIGACDASAKLMDVREGTCRQTFGHSDDINAIKCFPNGEA 240
QY 241 ICTGSDASCRLFDLRADQELICFHSHTICGITSVAFLSGRLLEAGYDDFNCNVWDSM 300
Db 241 ICTGSDASCRLFDLRADQELICFHSHTICGITSVAFLSGRLLEAGYDDFNCNVWDSM 300
QY 301 KSERVGLSGHNRVSCIGVTADGMVATGSDSFLKIMN 340
Db 301 KSERVGLSGHNRVSCIGVTADGMVATGSDSFLKIMN 340

RESULT 5
GBB1_HUMAN STANDARD; PRT; 340 AA.
ID GBB1_HUMAN
AC P04901; P04697;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1
DE (TRANSDUCIN BETA CHAIN 1).
GN GNB1.
OS Homo sapiens (Human), Mus musculus (Mouse), Bos taurus (Bovine), and
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606, 10090, 9913, 9615;
RN 11
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Liver;
RX MEDLINE=87030912; PubMed=3095147;
RA Codina J., Stengel D., Woo S.L.C., Birnbaumer L.;
RT "Beta-subunits of the human liver Gs/Gi signal-transducing proteins
RT and those of bovine retinal rod cell transducin are identical.";
RL FEBS Lett. 207:187-192(1986).
RN 12
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; TISSUE=Adrenal gland;
RA Qiu R., Schlumber B.P.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine;
RX MEDLINE=86177563; PubMed=3083416;
RA Fong H.K.W., Hurley J.B., Hopkins R.S., Make-Lye R., Johnson M.S.,
RA Doolittle R.F., Simon M.I.;

```

```

RT "Repetitive segmental structure of the transducin beta subunit:
RT homology with the CDC4 gene and identification of related mRNAs.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:2162-2166(1986).
RN 14
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine;
RX MEDLINE=86030675; PubMed=2414128;
RA Sugimoto K., Nakada T., Tanabe T., Takahashi H., Noda M., Minamino N.,
RA Kangawa K., Matsuo H., Hirose T., Inayama S., Numa S.;
RT "Primary structure of the beta-subunit of bovine transducin deduced
RT from the cDNA sequence.";
RL FEBS Lett. 191:235-240(1985).
RN 15
RP SEQUENCE FROM N.A.
RC SPECIES=Canis familiaris;
RX MEDLINE=97445667; PubMed=9300552;
RA Kyima T., Paulin L., Hurwitz M.Y., Hurwitz R.L., Komonen B.;
RT "Cloning of the cDNA encoding rod photoreceptor
RT cGMP-phosphodiesterase alpha and gamma subunits from the retinal
RT degenerate Labrador retriever dog.";
RL Res. Vet. Sci. 62:293-296(1997).
RN 16
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF HETEROTRIMER.
RX MEDLINE=96107343; PubMed=8521505;
RA Wall M.A., Coleman D.E., Lee E., Iniguez-Lluhi J.A., Posner B.A.,
RA Gilman A.G., Sprang S.R.;
RT "The structure of the G protein heterotrimer Gi alpha 1 beta 1 gamma
RT 2.";
RL Cell 83:1047-1058(1995).
RN 17
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF BETA-GAMMA DIMER.
RX MEDLINE=96149254; PubMed=8552196;
RA Sondek J., Bohm A., Lambright D.G., Hamm H.E., Sigler P.B.;
RT "Crystal structure of a G-protein beta gamma dimer at 2.1-A
RT resolution.";
RL Nature 379:369-374(1996).
RN 18
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH PHOSDUCIN.
RX MEDLINE=98416696; PubMed=9739091;
RA Loew A., Ho Y.K., Blundell T., Bax B.;
RT "Phosducin induces a structural change in transducin beta gamma.";
RL Structure 6:1007-1019(1998).
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
CC EFFECTOR INTERACTION.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X04526; CAA28207.1; -
DR EMBL; U29055; AAC52905.1; -
DR EMBL; X03073; CAA26875.1; -
DR EMBL; M13236; AAA30792.1; -
DR EMBL; M36430; AAA63265.1; -
DR EMBL; Z75134; CAA99446.1; -
DR PIR; A24853; RGHUB1.
DR PIR; A24225; RGOB01.
DR PDB; 1GG2; 12-FEB-97.
DR PDB; 1GP2; 12-FEB-97.
DR PDB; 1TBG; 01-APR-97.
DR PDB; 1AOR; 16-FEB-99.
DR PDB; 1B9X; 23-FEB-99.
DR PDB; 1B9Y; 23-FEB-99.
DR MM; 139380; -

```

DR MGD; MGI:95781; Gmb1.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family; 3D-structure.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT CONFLICT 71 71 V -> L (IN REF. 4).
 SQ SEQUENCE 340 AA; 37377 MW; 896CBD32D2686598 CRC64;

Query Match 87.2%; Score 1578; DB 1; Length 340;
 Best Local Similarity 83.2%; Pred. No. 3.8e-132;
 Matches 283; Conservative 32; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGEMQLRQEAQLKQIADARKACADVTIAELVSGLEVGRVQVMTTRRLRGLAKIYA 60
 1 MSELQDLRQEAQLKQIRDAKACADATISQITNNIDPVGRIOVRTRLRGLAKIYA 60
 QY 61 MHWATDSKLVASQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGLDNI 120
 61 MHWGTDSRLVSAQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNYVACGLDNI 120
 QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCGRFLDNNIVTSSGDTTCALWDIETGQKTVF 180
 121 CSIYNLKTREGNVKVSRELGHGTGYLSCGRFLDNNIVTSSGDTTCALWDIETGQKTVF 180
 Db 121 CSIYNLKTREGNVKVSRELGHGTGYLSCGRFLDNNIVTSSGDTTCALWDIETGQKTVF 180
 QY 181 VGHGDCMSLAVSPDFNLFIISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
 181 TGHGDMVMSLAPDTRFLVSGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
 Db 241 TGHGDMVMSLAPDTRFLVSGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELICFSHESIIGITSVAFLSGRLIFAGYDDFNQVWDSM 300
 241 FATGSDATCRFLDLRADQELIMTYSHDNIIGITSVSFSKSGRLIFAGYDDFNQVWDSM 300
 Db 241 FATGSDATCRFLDLRADQELIMTYSHDNIIGITSVSFSKSGRLIFAGYDDFNQVWDSM 300
 QY 301 KSERVILSGHDNRVSCGLVTADGMAVATGSWDSFLKIWN 340
 301 KADRAVLAGHDNRVSCGLVTDDGMAVATGSWDSFLKIWN 340
 Db 301 KADRAVLAGHDNRVSCGLVTDDGMAVATGSWDSFLKIWN 340

RESULT 6
 GBB1_XENLA STANDARD; PRT; 340 AA.
 AC P79959;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1
 DE (TRANSDUCIN BETA CHAIN 1) (XGBETA1).
 GN GNB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97109512; PubMed=8951792;
 RA Devic E., Paquereau L., Rizzoti K., Monier A., Knibiehler B.,
 RA Audigier Y.;
 RT "The mRNA encoding a beta subunit of heterotrimeric GTP-binding
 RT proteins is localized to the animal pole of Xenopus laevis oocyte and
 RT embryos.";

RL Mech. Dev. 59:141-151(1996).
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This Swiss-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X86969; CAA60532.1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37330 MW; DE036FEF60A2D6A9 CRC64;

Query Match 87.0%; Score 1573; DB 1; Length 340;
 Best Local Similarity 82.9%; Pred. No. 1.1e-131;
 Matches 282; Conservative 31; Mismatches 27; Indels 0; Gaps 0;

QY 1 MGEMQLRQEAQLKQIADARKACADVTIAELVSGLEVGRVQVMTTRRLRGLAKIYA 60
 1 MSELQDLRQEAQLKQIRDAKACADATLAQITANIDPVGRIOVRTRLRGLAKIYA 60
 Db 1 MSELQDLRQEAQLKQIRDAKACADATLAQITANIDPVGRIOVRTRLRGLAKIYA 60
 QY 61 MHWATDSKLVASQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGLDNI 120
 61 MHWGTDSRLVSAQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNYVACGLDNI 120
 Db 61 MHWGTDSRLVSAQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNYVACGLDNI 120
 QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCGRFLDNNIVTSSGDTTCALWDIETGQKTVF 180
 121 CSIYNLKTREGNVKVSRELGHGTGYLSCGRFLDNNIVTSSGDTTCALWDIETGQKTVF 180
 Db 121 CSIYNLKTREGNVKVSRELGHGTGYLSCGRFLDNNIVTSSGDTTCALWDIETGQKTVF 180
 QY 181 VGHGDCMSLAVSPDFNLFIISGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
 181 TGHGDMVMSLAPDSRCFVSGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
 Db 181 TGHGDMVMSLAPDSRCFVSGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELICFSHESIIGITSVAFLSGRLIFAGYDDFNQVWDSM 300
 241 FATGSDATCRFLDLRADQELIMTYSHDNIIGITSVAFLSGRLIFAGYDDFNQVWDSM 300
 Db 241 FATGSDATCRFLDLRADQELIMTYSHDNIIGITSVAFLSGRLIFAGYDDFNQVWDSM 300
 QY 301 KSERVILSGHDNRVSCGLVTADGMAVATGSWDSFLKIWN 340
 301 KADRAVLAGHDNRVSCGLVTDDGMAVATGSWDSFLKIWN 340
 Db 301 KADRAVLAGHDNRVSCGLVTDDGMAVATGSWDSFLKIWN 340

RESULT 7
 GBB1_RAT STANDARD; PRT; 340 AA.
 ID GBB1_RAT
 AC P54311;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1
 DE (TRANSDUCIN BETA CHAIN 1).
 GN GNB1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Brain;
 RA Kuroda S., Tokunaga C., Konishi H., Kikkawa U.;
 RL Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U34958; AAC72249.1; -.
 DR HSSP; P04901; ITBG.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 DR Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37393 MW; 89755AACB2686598 CRC64;

Query Match 86.9%; Score 1572; DB 1; length 340;
 Best Local Similarity 83.2%; Pred. No. 1.3e-131;
 Matches 283; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAQLKQIADARKACADVTLAELVSGLEVGRVQMTTRTLRGHLAKIYA 60
 DB 1 MSELQQLRQEAQLKQIADARKACADATLSQITNNIDPYGRIQMTTRTLRGHLAKIYA 60

QY 61 MHWAIDSKLLVSASQDGLIWDSTYTNKVAIPLRSSWMTCAVPSGNFVACGIDNM 120
 DB 61 MHWGTDLSRLVVSASQDGLIWDSTYTNKVAIPLRSSWMTCAVPSGNVYACGIDNI 120

QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQKTVF 180
 DB 121 CSIYNLKTREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQKTVF 180

QY 181 VGHGDCMSLAVSPDENLFTSGACDASAKLMDVREGTCRQFTGHSIDINAIICFPNGEA 240
 DB 181 TGHGDMVSLAVSPDENLFTSGACDASAKLMDVREGTCRQFTGHSIDINAIICFPNGEA 240

QY 241 ICTGSDASCRFLDLRADQELICFSHESIIGITSVAFSGRLLFAGYDDFNQVWDSM 300
 DB 241 FATGSDATCRFLDLRADQELMTYSHDNIICGITSVSFSGRLLLAGYDDFNQVWDAAL 300

QY 301 KSERVILSGHDNRVSLGVTADGMVAATGSMDSFLKIWN 340
 DB 301 KADRAGDLAGHDNRVSLGVTDDGMVAATGSMDSFLKIWN 340

RESULT 8
 ID GBB2_HUMAN STANDARD; PRT; 340 AA.
 AC P11016;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 2
 DE (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT).
 GN GNB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87231903; PubMed=3108879;
 RA Fong H.K.W., Amatruda T.T. III, Birren B.W., Simon M.I.;
 RT "Distinct forms of the beta subunit of GTP-binding regulatory
 RT proteins identified by molecular cloning."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3792-3796(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87317607; PubMed=3114742;
 RA Gao B., Gilman A.G., Robishaw J.D.;
 RT "A second form of the beta subunit of signal-transducing G proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6122-6125(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99018118; PubMed=9799793;
 RA Gloeckner G., Scherer S., Schattevoy R., Boright A., Weber J.,
 RA Tsui L.-C., Rosenthal A.;
 RT "Large-scale sequencing of two regions in human chromosome 7q22:
 RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
 RT reveals 17 genes."
 RL Genome Res. 8:1060-1073(1998).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M16514; AAA03179.1; -.
 DR EMBL; M36429; AAA63264.1; -.
 DR EMBL; M16538; AAA35922.1; ALT_SEQ.
 DR EMBL; AF053356; AAC78794.1; -.
 DR PIR; B26617; RGHUB2.
 DR HSSP; P04901; ITBG.
 DR MIM; 139390; -.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.

Transducer; Repeat; WD repeat; Multigene family.

FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT CONFLICT 195 195 D -> N (IN REF. 2).
 SQ SEQUENCE 340 AA; 37331 MW; 5D08FFA240ADEEE6 CRC64;

Query Match 84.5%; Score 1528; DB 1; Length 340;
 Best Local Similarity 80.9%; Pred. No. 1e-127;
 Matches 275; Conservative 31; Mismatches 34; Indels 0; Gaps 0;

OY 1 MGEMEQLRQAEQLKKQIADARKACADVTLLAELVSGLEVGRVQMRTRTLRGLAKIYA 60
 1 MSELQRLQAEQLRQIADARKACADGDTLTQITAGLDPVGRIO MRTRTLRLGLAKIYA 60

OY 61 MHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAAYAPSGNEVACGGLDNI 120
 61 MHWGTDSRLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAAYAPSGNEVACGGLDNI 120

OY 121 CSIYNLKSREGNVKVSRELSTAHNTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQQTVE 180
 121 CSYSLKTRREGNVKVSRELSTAHNTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQQTVE 180

OY 181 VGHGDCMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTGHESDINAIICFPNGEA 240
 181 AGHSGDVMSLSLAPDGRFTVSGACDASIKLMDVDRSMCRQFTGHESDINAVAFPPNGYA 240

OY 241 ICTGSDASCRFLDLRADQELICFESHESIIGITSVAFSLSGRLLFAGYDDFNCNWDSM 300
 241 FTTGSDATCRLFLDLRADQELIMYSHDNIICGITSVAFSRSGRLLAGYDDFNCNWDAM 300

OY 301 KSERVGLSGHDNRVSCIGVTADGMAVATGWSDFLKIWN 340
 301 KGRAGVLAGHDNRVSCIGVTDDGMAVATGWSDFLKIWN 340

Db

RESULT 9
 GBB2_MOUSE STANDARD; PRT; 340 AA.

AC P54312;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(S)/G(T) BETA SUBUNIT 2
 DE (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT).
 GN GNB2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/KAPLAN;
 RA Kuroda S., Tokunaga C., Konishi H., Kikkawa U.;
 RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 182-297 FROM N.A.
 RC STRAIN=CF1;
 RX MEDLINE=97011591; PubMed=8858601;
 RA Williams C.J., Schultz R.M., Kopf G.S.;
 RT "G protein gene expression during mouse oocyte growth and maturation,
 and preimplantation embryo development.";
 RL Mol. Reprod. Dev. 44:315-323(1996).
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.

CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN MEIOTICALLY INCOMPETENT OOCYTES.
 CC EXPRESSION INCREASES IN FULLY GROWN MEIOTICALLY COMPETENT OOCYTES.
 CC EXPRESSION THEN DECREASES DURING METAPHASE-II ARRESTED EGGS, ONE-
 CC CELL EMBRYO, TWO-CELL EMBRYO AND EIGHT-CELL EMBRYO STAGES, AND
 CC INCREASES AGAIN DURING BLASTOCYST STAGE.
 CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; U34960; AAC72250.1; -.
 DR EMBL; U38505; AAB01736.1; -.
 DR HSSP; P04901; ITBG.
 DR MGD; MGI:95784; Gnb2.
 DR InterPro; IPR001632; -.
 DR InterPro; IPR001680; -.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 DR Transducer; Repeat; WD repeat; Multigene family; Polymorphism.

FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 FT VARIANT 248 248 S -> A (IN STRAIN CF1).
 SQ SEQUENCE 340 AA; 37333 MW; FEC7DB4F9B43737D CRC64;

Query Match 84.1%; Score 1521; DB 1; Length 340;
 Best Local Similarity 80.3%; Pred. No. 4.2e-127;
 Matches 273; Conservative 32; Mismatches 35; Indels 0; Gaps 0;

OY 1 MGEMEQLRQAEQLKKQIADARKACADVTLLAELVSGLEVGRVQMRTRTLRGLAKIYA 60
 1 MSELQRLQAEQLRQIADARKACADGDTLTQITAGLDPVGRIO MRTRTLRLGLAKIYA 60

OY 61 MHWATDSKLLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAAYAPSGNEVACGGLDNI 120
 61 MHWGTDSRLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAAYAPSGNEVACGGLDNI 120

OY 121 CSIYNLKSREGNVKVSRELSTAHNTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQQTVE 180
 121 CSYSLKTRREGNVKVSRELSTAHNTGYLSCCRFLDNNIVTSSGDTTCALWDIETGQQTVE 180

OY 181 VGHGDCMSLAVSPDFNLFIGACDASAKLMDVREGTCRQFTGHESDINAIICFPNGEA 240
 181 AGHSGDVMSLSLAPDGRFTVSGACDASIKLMDVDRSMCRQFTGHESDINAVAFPPNGYA 240

OY 241 ICTGSDASCRFLDLRADQELICFESHESIIGITSVAFSLSGRLLFAGYDDFNCNWDSM 300
 241 FTTGSDATCRLFLDLRADQELIMYSHDNIICGITSVAFSRSGRLLAGYDDFNCNWDAM 300

OY 301 KSERVGLSGHDNRVSCIGVTADGMAVATGWSDFLKIWN 340
 301 KGRAGVLAGHDNRVSCIGVTDDGMAVATGWSDFLKIWN 340

Db

RESULT 10
 GBB1_CABEL STANDARD; PRT; 340 AA.

AC P17343; Q19394;

CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z23105; CAA80652.1; -.
 CC HSSP; P04901; 1GP2.
 CC InterPro; IPR001632; -.
 CC InterPro; IPR001680; -.
 CC Pfam; PF00400; WD40; 7.
 CC PRINTS; PR00319; GPROTEINB.
 CC PRINTS; PR00320; GPROTEINBPT.
 CC PROSITE; PS00678; WD_REPEATS_1; 2.
 CC PROSITE; PS50082; WD_REPEATS_2; 5.
 CC PROSITE; PS50294; WD_REPEATS_REGION; 1.
 CC Transducer; Repeat; WD repeat.
 FT REPEAT 54 84 WD 1.
 FT REPEAT 96 126 WD 2.
 FT REPEAT 142 171 WD 3.
 FT REPEAT 183 213 WD 4.
 FT REPEAT 225 255 WD 5.
 FT REPEAT 269 299 WD 6.
 FT REPEAT 311 341 WD 7.
 SQ SEQUENCE 341 AA; 37320 MW; 4A2662588387592E CRC64;

Query Match 81.8%; Score 1480; DB 1; Length 341;
 Best Local Similarity 79.6%; Pred. No. 1.8e-123;
 Matches 269; Conservative 30; Mismatches 39; Indels 0; Gaps 0;

QY 3 EMEQLRQEAQLKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYAMH 62
 DB 4 DLEALRQETEQLKQIREARKAGDTTLAQACSGEAVGRIQMRTRRLRGLAKIYAMH 63
 QY 63 WATDSKLLVASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNEVACGGIDNMCS 122
 DB 64 WASDSRLVSAQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNEVACGGIDNMCS 123
 QY 123 IYNLKSREGNVKYSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVFVG 182
 DB 124 IYSLKTRREGNVKYSRELPGHTGYLSCCRFLDDNNIVTSSGDMSCALWDIETGQOKTVFVG 183
 QY 183 HTGDCMSLAVSPDENLFIAGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEATC 242
 DB 184 HTGDMVSLSTSPDFTFVSGACDASAKLMDVREGTCROTFTGHESDINAIITFPNGHAF 243
 QY 243 TGSDDASCRFLDLRADQELICFSHESIICGITSVAFLSGRLFAGYDDFNCNVWDSMKS 302
 DB 244 TGSDDATCRLFLRADQELIGMYSHDNITIGITSVAFSKSGRLLGHYDDFNCNVWDLKQ 303
 QY 303 ERVGIISGHNDNRVSLGVLTADGMVATGSDSFLKIWN 340
 DB 304 ETHGVLAGHNDNRVSLGVLTEDGSAVATGSDSFLKIWN 341

RESULT 14
 GBB1_HOMAM STANDARD; PRT; 340 AA.
 AC 045040;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1
 (TRANSDUCIN BETA CHAIN 1).

GN GBETAL.
 OS Homarus americanus (American lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Nephropoidea; Nephropidae; Homarus.
 OX NCBI_TaxID=6706;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98410740; PubMed=9740024;
 RA Xu F., Hollins B., Landers T.M., McClintock T.S.;
 RT "Molecular cloning of a lobster Gbeta subunit and Gbeta expression in
 RT olfactory receptor neuron dendrites and brain neuropil."
 RL J. Neurobiol. 36:525-536(1998).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF044735; AAC02998.1; -.
 CC InterPro; IPR001632; -.
 CC InterPro; IPR001680; -.
 CC Pfam; PF00400; WD40; 7.
 CC PRINTS; PR00319; GPROTEINB.
 CC PRINTS; PR00320; GPROTEINBPT.
 CC PROSITE; PS00678; WD_REPEATS_1; 3.
 CC PROSITE; PS50082; WD_REPEATS_2; 6.
 CC PROSITE; PS50294; WD_REPEATS_REGION; 1.
 CC Transducer; Repeat; WD repeat; Multigene family.
 FT REPEAT 53 83 WD 1.
 FT REPEAT 95 125 WD 2.
 FT REPEAT 141 170 WD 3.
 FT REPEAT 182 212 WD 4.
 FT REPEAT 224 254 WD 5.
 FT REPEAT 268 298 WD 6.
 FT REPEAT 310 340 WD 7.
 SQ SEQUENCE 340 AA; 37409 MW; 3483245F9291D82E CRC64;

Query Match 81.8%; Score 1479; DB 1; Length 340;
 Best Local Similarity 78.2%; Pred. No. 2.1e-123;
 Matches 266; Conservative 35; Mismatches 39; Indels 0; Gaps 0;

QY 1 MGEMQLRQEAQLKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
 DB 1 MNDLDSLRLQEAERLKNITIRARKNALDTLVQATAGMDPIGRIQMRTRRLRGLAKIYA 60
 QY 61 MHMATDSKLLVASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNEVACGGIDNM 120
 DB 61 MHMGDSRLVSAQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNEVACGGIDNI 120
 QY 121 CSYINLKSREGNVKYSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALWDIETGQOKTVF 180
 DB 121 CSYISLKTREGNVKYSRELPGHTGYLSCCRFLDDNNIVTSSGDMTCALWDIETGQOKTVF 180
 QY 181 VGHGDCMSLAVSPDENLFIAGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEATC 240
 DB 181 TGHGDMVSLSTSPNMRFTSGACDASAKLMDIRDMCRQOTFTGHESDINAVTFFPNHGA 240
 QY 241 ICTGSDASCRFLDLRADQELICFSHESIICGITSVAFLSGRLFAGYDDFNCNVWDSM 300
 DB 241 FATGSDATCRLFLRADQELAMYSHDNITIGITSVAFSKSGKILLAGYDDFNCNVWDSM 300

QY 301 KSERVILSGHNDNRVSLGVTADGMATGSDSFLKIWN 340
 Db 301 RTERAGVLACHDNRVSLCLGVTEDGMATGSDSFLKIWN 340

RESULT 15
 GBB2_BOVIN STANDARD; PRT; 326 AA.

AC P11017;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 2
 DE (TRANSDUCIN BETA CHAIN 2) (G PROTEIN BETA 2 SUBUNIT) (FRAGMENT).
 GN GNB2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87231903; PubMed=3108879;
 RA Fong H.K.W., Amatruda T.T. III, Birren B.W., Simon M.I.;
 RT "Distinct forms of the beta subunit of GTP-binding regulatory
 RL proteins identified by molecular cloning.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3792-3796(1987).
 RN [2]
 RP SEQUENCE OF 88-302 FROM N.A.
 RX MEDLINE=87317607; PubMed=3114742;
 RA Gao B., Gilman A.G., Robishaw J.D.;
 RT "A second form of the beta subunit of signal-transducing G proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6122-6125(1987).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
 CC EFFECTOR INTERACTION.
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; M16480; AAA30553.1; -;
 DR EMBL; M36431; AAA62717.1; -;
 DR EMBL; M16539; AAA30552.1; -;
 DR PIR; A26617; RGOB02.
 DR HSSP; P04901; 1GP2.
 DR InterPro; IPR001680; -;
 DR Pfam; PF00400; WD40; 7.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Transducer; Repeat; WD repeat; Multigene family.
 FT NON_TER 1
 FT REPEAT 39 69 WD 1.
 FT REPEAT 81 111 WD 2.
 FT REPEAT 127 156 WD 3.
 FT REPEAT 168 198 WD 4.
 FT REPEAT 210 240 WD 5.
 FT REPEAT 254 284 WD 6.
 FT REPEAT 296 326 WD 7.
 FT REPEAT 271 271 WD 7.
 SQ SEQUENCE 326 AA; 35645 MW; EE9B0EFF5BCC51B23 CRC64;

Query Match 81.2%; Score 1469; DB 1; Length 326;

Best Local Similarity 80.7%; Pred. No. 1.6e-122;
 Matches 263; Conservative 30; Mismatches 33; Indels 0; Gaps 0;
 QY 15 KKQIADARKACADVTTLAEVSGLEVGRVQMRTRRLRGLAKIYAMHMATDSKLLVSAS 74
 Db 1 RNQIRDARKACGDSITLQITAGLDPVGRIQMRTRRLRGLAKIYAMHMATDSKLLVSAS 60
 QY 75 QDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNMCSTYLNKSRGNV 134
 Db 61 QDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNMCSTYLNKSRGNV 120
 QY 135 VSRELTAHTGYLSCCRFLDNNIVTSSGDTTCALMDIETGQKTVFVHTGDCMSLAVSP 194
 Db 121 VSRELPGHTGYLSCCRFLDNNIITSSGDTTCALMDIETGQKTVFVHTGDCMSLAVSP 180
 QY 195 DENLFISGACDASAKLMDVREGTCRQTFTHGSDINAIICFPNGEALCTGSDASCRLFD 254
 Db 181 DGRTFVSGACDASIKLMDVDSMCRQTFTHGSDINAVAFPNGYAFTTGSDDATCRLFD 240
 QY 255 LRADQELICFSHESIIGITSVAFLSGRLIFAGYDDFNCNWDMSKRSRVGILSGHNR 314
 Db 241 LRADQELLMYSHDNIIGITSVAFLSGRLLAGYDDFNCNWDMSKRSRVGILSGHNR 300
 QY 315 VSCLGVTADGMATGSDSFLKIWN 340
 Db 301 VSCLGVTDDGMATGSDSFLKIWN 326

Search completed: September 28, 2001, 10:34:29
 Job time: 284 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2001, 10:34:00 (without alignments)
1182.537 Million cell updates/sec

```

Title: US-09-492-029-5
Perfect score: 1809
Sequence: 1 MGENEQLROAEQLKKQIAD.....TADGMAVATGWSDFLKIWN 340

```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```

post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```

SPTREMBL_16:*
1:  sp_archaea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:  sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp Vertebrate:*
14: sp_virus:*

```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match.	Length	DB	ID	Description
1	1670	92.3	340	13	Q9DFG9	Q9dfg9 ambystoma t
2	1575	87.1	340	13	Q9DFH0	Q9dfh0 ambystoma t
3	1563	86.4	340	11	Q9QW8	Q9qwg8 rattus norv
4	1516	83.8	340	4	Q9HAV0	Q9hav0 homo sapien
5	1503	83.1	340	11	Q9JHX8	Q9jhx8 mus musculu
6	1252	69.2	352	3	Q9J387	Q9j387 cryptococcu
7	1226.5	67.8	347	3	Q9HFS3	Q9hfs3 pneumocysti
8	1219.5	67.4	352	3	Q74214	Q74214 emericeila
9	967.5	53.5	358	5	Q9W3J1	Q9w3j1 drosophila
10	949.5	52.5	395	5	Q9H4U9	Q9h4u9 homo sapien
11	831	45.9	346	5	Q9NFZ1	Q9nfm1 calliphora
12	820.5	45.4	377	10	Q9XFK0	Q9xfk0 pisum sativ
13	819	45.3	377	10	Q9SW94	Q9sw94 pisum sativ
14	814	45.0	346	5	Q9VM29	Q9vw29 drosophila
15	809	44.7	377	10	Q9FV61	Q9fv61 nicotiana t
16	794	43.9	380	10	O64944	O64944 avena fatuaa
17	743.5	41.1	283	4	Q9UFT3	Q9uft3 homo sapien
18	689.5	38.1	436	3	Q9Y7B8	Q9y7b8 kluyveromyc
19	584	37.8	186	5	O45041	O45041 homarus ame

20	635	35.1	371	5	Q9XZV6	Q9XZV6 geodia cydo
21	609	33.7	123	11	Q61621	Q61621 mus musculus
22	585.5	32.4	240	10	Q40456	Q40456 nicotiana t
23	317	17.5	1241	2	Q9XBD8	Q9XBD8 amycolatops
24	308	17.0	333	10	Q9SY00	Q9SY00 arabidopsis
25	305.5	16.9	502	3	Q74855	Q74855 schizosach
26	304	16.8	522	4	Q43445	Q43445 homo sapien
27	303	16.7	579	5	Q76734	Q76734 dictyostell
28	300.5	16.6	485	4	Q9NVX2	Q9NVX2 homo sapien
29	300.5	16.6	561	3	Q14432	Q14432 schizosach
30	300.5	16.6	586	3	Q9UUG8	Q9UUG8 schizosach
31	300	16.6	520	4	Q43864	Q43864 homo sapien
32	299	16.5	1049	4	Q9ZEM4	Q9ZEM4 streptomyce
33	299	16.5	1676	2	Q9KXX9	Q9KXX9 streptomyce
34	296	16.4	521	4	Q43172	Q43172 homo sapien
35	295.5	16.3	318	5	Q96653	Q96653 trypanosoma
36	294.5	16.3	317	13	Q9W711	Q9W711 xenopus lae
37	294	16.3	334	4	Q9NWX7	Q9NWX7 homo sapien
38	292	16.1	473	10	Q9FLX9	Q9FLX9 arabidopsis
39	287	15.9	587	5	Q44083	Q44083 caenorhabdi
40	284.5	15.7	476	13	Q93531	Q93531 xenopus lae
41	283.5	15.7	481	5	Q9VPR4	Q9VPR4 drosophila
42	282	15.6	381	5	Q9U4Y2	Q9U4Y2 eupyryma sc
43	281.5	15.6	330	4	Q9NUL4	Q9NUL4 homo sapien
44	280	15.5	553	5	Q9VVI0	Q9VVI0 drosophila
45	279.5	15.5	480	5	Q96995	Q96995 drosophila

ALIGNMENTS

```

RESULT      1
09DFG9
ID      09DFG9      PRELIMINARY;      PRT;      340 AA.
AC      09DFG9;
DT      01-MAR-2001 (TREMblrel. 16, Created)
DT      01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT      01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE      G-PROTEIN B3 SUBUNIT.
OS      Ambystoma tigrinum (Tiger salamander).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
OC      Ambystoma.
OX      NCBI_TaxID=8305;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=RETINA;
RA      Ryan J.C., Crouch R.K., Ma J.;
RT      "Cloning and Characterization of G-protein Beta subunits from the
RL      Salamander Retina.";
DR      Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
SQ      EMBL; AF277162; AAG31061.1; -.
      SEQUENCE      340 AA;      37355 MW;      6C284C1100552DBE CRC64;

```

	Query Match	92.3%;	Score 1670;	DB 13;	Length 340;	
	Best Local Similarity	88.8%;	Pred. No. 5.1e-148;			
	Matches 302;	Conservative	23;	Mismatches 15;	Indels	Gaps
QY	1 MGEMEQLRQEAEOLKKQIADARKACADVTLAELVSGLEVGVRVQMRTTRTLRGHLAKIYA	60				
Dd	1 MCGMEQLRQEAEOLKKQIAEARKVCADTTLAQITAGMEVNGRIQMRTRTLRLGHLAKIYA	60				
QY	61 MHMATDSKLLVASASODGLIWMDSYTTNKNVHAIPLRSSWMTCAIAPSGNFVACGGLDNM	120				
Dd	61 MHWSNDSRLVASASODGLIWMDTYSTNKVHAIPLRSSWMTCSYAPSGNFVACGGLDNM	120				
QY	121 CSTYNLKSREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGOOKTVF	180				
Dd	121 CSILNLKTREGNVKVSRELAHNTGYLSCCRFLDDNQIVTSSDGTTCALMDIETGOOKTVF	180				
QY	181 VGHGTDCMSLAVSPDENLFISGACDASAKIMDVREGTCROFTTGHSIDINAICEFPNGEA	240				

Db 181 MHTGDCMSLAVSPDFRIFVSGACDATAKLMDIRECTCRQTFTHGHSIDINAIICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELICFSHESITICITSVAFSLSGRLIFAGYDDFNCNVWDSM 300
 Db 241 VCTGSDATCRLFDLRADQELTVSHESITICITSVAFSRSGRLLAGYDDFNCNVWDSM 300
 QY 301 KSERVGLSGHDNRVSCIGVTADGMVAATGSDSFLKIWN 340
 Db 301 KGERVGLSGHDNRVSCIGVTADGMVAATGSDSFLKIWN 340

RESULT 2

Q9DFHO PRELIMINARY; PRT; 340 AA.
 AC Q9DFHO;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE G-PROTEIN B1 SUBUNIT.
 OS Ambystoma tigrinum (Tiger salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Ambystomatidae;
 OC Ambystoma.
 OX NCBI_TaxID=8305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=RETINA;
 RA Ryan J.C., Crouch R.K., Ma J.;
 RT "Cloning and Characterization of G-protein Beta subunits from the
 RL Salamander Retina."
 RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF277161; AAG31060.1;
 SQ SEQUENCE 340 AA; 37332 MW; 84E1451FDD83D8F3 CRC64;

Query Match 87.1%; Score 1575; DB 13; Length 340;
 Best Local Similarity 82.9%; Pred. No. 3.9e-139;
 Matches 282; Conservative 31; Mismatches 27; Indels 0; Gaps 0;

QY 1 MGEMEQLRQAEQKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
 Db 1 MSELQRLQAEQKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
 QY 61 MHMATDSKLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 Db 61 MHMTDSRLVSVASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 QY 121 CSIYNLKSREGNVKVSRELSTHTGYLSCCRFLDNNITVSSGDTTCALMDIETGQQTTF 180
 Db 121 CSIYNLKSREGNVKVSRELSTHTGYLSCCRFLDNNITVSSGDTTCALMDIETGQQTTF 180
 QY 181 VGHGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCRQTFTHGHSIDINAIICFPNGEA 240
 Db 181 AGHTGDVMSLSLAPDSRCFVSGACDASAKLMDVREGTCRQTFTHGHSIDINAIICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELICFSHESITICITSVAFSLSGRLIFAGYDDFNCNVWDSM 300
 Db 241 FATGSDATCRLFDLRADQELMTYSHDNITICITSVAFSRSGRLLAGYDDFNCNVWDSM 300
 QY 301 KSERVGLSGHDNRVSCIGVTADGMVAATGSDSFLKIWN 340
 Db 301 KADRAVGLAGHDNRVSCIGVTADGMVAATGSDSFLKIWN 340

RESULT 3

Q9QWG8 PRELIMINARY; PRT; 340 AA.
 AC Q9QWG8;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DE G-PROTEIN BETA SUBUNIT.
 GN RGB1.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Wang X.B., Funada M., Imai Y., Revey R.S., Ujike H., Vandenbergh D.J.,
 RA Uhl G.R.;
 RT "Rgd1: A psychostimulant-regulated gene essential for establishing
 RT cocaine sensitization."
 RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RL EMBL; U88324; AAD00650.1;
 DR HSSP; P04901; 1TBG.
 DR InterPro; IPR001632;
 DR InterPro; IPR001680;
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00319; GPROTEINB.
 DR PRINTS; PR00320; GPROTEINBPT.
 DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
 DR SMART; SM00320; WD40; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 340 AA; 37387 MW; D9EBEC6B0FF7EC57 CRC64;

Query Match 86.4%; Score 1563; DB 11; Length 340;
 Best Local Similarity 82.4%; Pred. No. 5.1e-138;
 Matches 280; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

QY 1 MGEMEQLRQAEQKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
 Db 1 MSELQRLQAEQKQIADARKACADVTLAELVSGLEVGRVQMRTRRLRGLAKIYA 60
 QY 61 MHMATDSKLVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 Db 61 MHMTDSRLVSVASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
 QY 121 CSIYNLKSREGNVKVSRELSTHTGYLSCCRFLDNNITVSSGDTTCALMDIETGQQTTF 180
 Db 121 CSIYNLKSREGNVKVSRELSTHTGYLSCCRFLDNNITVSSGDTTCALMDIETGQQTTF 180
 QY 181 VGHGDCMSLAVSPDFNLFISGACDASAKLMDVREGTCRQTFTHGHSIDINAIICFPNGEA 240
 Db 181 TGHGTVMSLSLAPDTRLFVSGACDASAKLMDVREGTCRQTFTHGHSIDINAIICFPNGEA 240
 QY 241 ICTGSDASCRLFDLRADQELICFSHESITICITSVAFSLSGRLIFAGYDDFNCNVWDSM 300
 Db 241 FATGSDATCRLFDLRADQELMTYSHDNITICITSVAFSRSGRLLAGYDDFNCNVWDSM 300
 QY 301 KSERVGLSGHDNRVSCIGVTADGMVAATGSDSFLKIWN 340
 Db 301 NADRAVGLAGHDNRVSCIGVTADGMVAATGSDSFLKIWN 340

RESULT 4

Q9HAVO PRELIMINARY; PRT; 340 AA.
 AC Q9HAVO;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT 4.
 GN GNB4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Puhi H.L. III, Ikeda S.R., Aronstam R.S.;
 RT "Cloning and Characterization of Human G-protein Beta 4."
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF300648; AAG18442.1;

SQ SEQUENCE 340 AA; 37567 MW; EDF085155A1EDC89 CRC64;

Query Match 83.8%; Score 1516; DB 4; Length 340;
Best Local Similarity 79.7%; Pred. No. 1.3e-133;
Matches 271; Conservative 35; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAQKQIADARKACADVTIAELVSGLEVGRVQMRTRLRGLAKIYA 60
1 MSELQRLQEAQKQIADARKACADVTIAELVSGLEVGRVQMRTRLRGLAKIYA 60
QY 61 MHMATDSKLVSASQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
61 MHMGYDSRLVLSASQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQOKTVE 180
121 CSIYNLKTREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQOKTVE 180
QY 181 VGHGDCMSLAVSPDENLFIAGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
181 TGHSGDVMSLSLSPDMRTFVSGACDASSKLMIDRGMCROSFTGHVDINAVSFPNGYA 240
QY 241 ICTGSDDASCRLFDLRADQELICFSHESIIGITSVAFLSGLRLLFAGYDDFNCNWDSM 300
241 FATGSDDATCRLFDLRADQELLYSHDNIIGITSVAFLSGLRLLFAGYDDFNCNWDTL 300
QY 301 KSERVGLSGHNDNRVSLGVADGMVAVATGSWDSFLKIWN 340
301 KGDRAVGLAGHNDNRVSLGVADGMVAVATGSWDSFLKIWN 340
Db

RESULT 5
Q9JHX8 PRELIMINARY; PRT; 340 AA.
AC Q9JHX8; 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE G-PROTEIN BETA-4 SUBUNIT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Arnot M.I., Stotz S.C., Jarvis S.E., Zampont G.W.;
RT "differential modulation of N-type alpha 1B and P/Q-type alpha 1A
calcium channels by different G protein beta subunit isoforms.";
RT J. Physiol. 0:0-0(2000).
RL EMBL; AF277893; AAF82124.1; -.
DR InterPro; IPR001632; -.
DR InterPro; IPR001680; -.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00319; GPROTEINB.
DR PRINTS; PR00320; GPROTEINBRT.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
KW Repeat; WD repeat.
SQ SEQUENCE 340 AA; 37379 MW; F06827EBC2F0E966 CRC64;

Query Match 83.1%; Score 1503; DB 11; Length 340;
Best Local Similarity 79.1%; Pred. No. 2.1e-132;
Matches 269; Conservative 36; Mismatches 35; Indels 0; Gaps 0;

QY 1 MGEMEQLRQEAQKQIADARKACADVTIAELVSGLEVGRVQMRTRLRGLAKIYA 60
1 MSELQRLQEAQKQIADARKACADVTIAELVSGLEVGRVQMRTRLRGLAKIYA 60
QY 61 MHMATDSKLVSASQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
61 MHMGYDSRLVLSASQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNM 120
Db

QY 121 CSIYNLKSREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQOKTVE 180
121 CSIYNLKTREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQOKTVE 180
QY 181 VGHGDCMSLAVSPDENLFIAGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGEA 240
181 TGHSGDVMSLSLSPDLKTFVSGACDASSKLMIDRGMCROSFTGHISDINAVSFPNGYA 240
QY 241 ICTGSDDASCRLFDLRADQELICFSHESIIGITSVAFLSGLRLLFAGYDDFNCNWDSM 300
241 FATGSDDATCRLFDLRADQELLYSHDNIIGITSVAFLSGLRLLFAGYDDFNCNWDTL 300
QY 301 KSERVGLSGHNDNRVSLGVADGMVAVATGSWDSFLKIWN 340
301 KGRSGVLAGHNDNRVSLGVADGMVAVATGSWDSFLKIWN 340
Db

RESULT 6
Q93887 PRELIMINARY; PRT; 352 AA.
ID Q93887; 01-MAY-1999 (Tremblrel. 10, Created)
AC Q93887; 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE G-PROTEIN BETA SUBUNIT GPB1.
GN GPB1.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H99;
RA Wang P., Perfect J.R., Heitman J.;
RT "The G-protein beta subunit GPB1 is required for mating in
Cryptococcus neoformans and functions in a pathway distinct from the
alpha subunit GPB1.";
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF091120; AAD03596.1; -.
DR HSP; P04901; 1TBG.
DR InterPro; IPR001632; -.
DR InterPro; IPR001680; -.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00319; GPROTEINB.
DR PRINTS; PR00320; GPROTEINBRT.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
DR SMART; SM00320; WD40; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 352 AA; 37904 MW; 36CF4F16AA2C6AB5 CRC64;

Query Match 69.2%; Score 1252; DB 3; Length 352;
Best Local Similarity 65.1%; Pred. No. 6.3e-109;
Matches 222; Conservative 59; Mismatches 52; Indels 8; Gaps 1;

QY 8 RQEAQKQIADARKACADVTIAELVSGLEVGRVQMRTRLRGLAKIYAMHMTDS 67
12 RREADGLKRLRAARDQADTSLRAMATDTPPLRITLKAARLTKGLHAKIYALHMAADT 71
QY 68 KLLVSASQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNMCSIYNL 127
72 RHIVSASQDGLIWDATYTNKVAIPLRSSWMTCAVAPSGNLVACGGLDNVCSIYSLR 131
QY 128 -----SREGNVKVSRELSAHTGYLSCCRFLDDNNIVTSSGDTTCALMDIETGQOKTV 179
132 GAGPGAPGAPGGQVAVARELSAHSGLSCCRFLINDRQIVTSSGDMTCMLMDIETGQRTME 191
QY 180 FVGHGDCMSLAVSPDENLFIAGACDASAKLMDVREGTCROTFTGHESDINAIICFPNGE 239
192 FNDHTGDMCISLAPNANLFIAGACDASAKLMDIRTKAVQFTTGHESDINAVQFPNGD 251
QY 240 AICTGSDDASCRLFDLRADQELICFSHESIIGITSVAFLSGLRLLFAGYDDFNCNWDS 299

Db 252 AFATGSDDASCLEFDLRADRELNSIAHNLICGITSVAFSISGRVLFAGYDDYCNVMDT 311
QY 300 MKSERVGLSGHNDNRVSCLGVTADGMAVATGSDSFLKIWN 340
Db 312 LKGRIGVLAGHENRVSCMGVSGDVALCTGSDSLKIVMS 352

RESULT 7

Q9HFS3 PRELIMINARY; PRT; 347 AA.

AC 09HFS3; 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN 11
RP SEQUENCE FROM N.A.
RA Puri V., Park J.G., Limper A.H., Thomas C.F. Jr.
RT "The Pneumocystis carinii guanine nucleotide-binding protein beta
RT subunit."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF306565; AAG27720.1;
SQ SEQUENCE 347 AA; 38438 MW; FEE1495006E24882 CRC64;

Query Match 67.8%; Score 1226.5; DB 3; Length 347;
Best Local Similarity 66.9%; Pred. No. 1.5e-106;
Matches 222; Conservative 47; Mismatches 62; Indels 1; Gaps 1;

QY 9 QEAQOLKQIADARKACADVTIAELVSGLEVGRVQMRTRTLRGLAKIYAMHWATDSK 68
Db 15 KRAEYLKEIKKKKDELADTNLRSMAGTLDVIERLSIRVRYTLKGLAKIYAMHWSTDK 74
QY 69 LVSASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACGGLDMCSITNLS 128
Db 75 HLVSASQDGKLIWDAYTTRKTHAIPLRSSWMTCAVAPSGNFVACGGLDMCSITNLS 134
QY 129 REGNVKVSRELTAHTGYLSCRFLLDNNITVSSGDTTCALMDIETGQOKTVFVGHGDCM 188
Db 135 KDGHAKIARELMAHTGYLSCRFLLDNNITVSSGDTTCALMDIETGQOKTVFVGHGDCM 194
QY 189 SLAVSP-DFNLIFSGACDASAKLMDVREGTCRQFTGHESDINAICFPNGEALCTGSD 247
Db 195 SLIHPTNPNEFVSGACDAFAKIMDIRIGKSVQTFAGHESDINAVQYFPNGNAFATGSD 254
QY 248 ASCRLFDLRADQELICFSHESIICGITSVAFSLGRLPAGYDDFNCAVWDSMKSERVGI 307
Db 255 ASCRLFDVRADRELNQYSAANIMCGITISFSNSGRLLFRAGYDDFNCAVWDSMKSERVGI 314
QY 308 LSGHNDNRVSCLGVTADGMAVATGSDSFLKIWN 339
Db 315 LQGHNDNRVSCVSGKDRSLATGSDSLKIWN 346

RESULT 8

Q74214 PRELIMINARY; PRT; 352 AA.

AC 074214; 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE G-PROTEIN BETA SUBUNIT.
GN SFAD.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=5072;
RN 11

RP SEQUENCE FROM N.A.
RA Rosen S., Yu J.-H., Adams T.H.;
RT "Aspergillus nidulans flba suppressor sfad identifies the G-beta
RT subunit of a heterotrimeric G protein."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF056182; AAC33436.1;
DR HSSP; P04901; 1TBG.
DR InterPro; IPR001632;
DR InterPro; IPR001680;
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00319; GPROTEINB.
DR PRINTS; PR00320; GPROTEINBPT.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_3.
DR SMART; SM00320; WD40; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 352 AA; 38888 MW; 186A16886B4DF466 CRC64;

Query Match 67.4%; Score 1219.5; DB 3; Length 352;
Best Local Similarity 64.6%; Pred. No. 6.9e-106;
Matches 223; Conservative 50; Mismatches 65; Indels 7; Gaps 3;

QY 2 GEMEQ----LRQEAQOLKQIADARKACADVTIAELVSG-LEVGRVQMRTRTLRGLH 55
Db 6 GEQMAKITAARREAEGLKDKIRRKDDIADTTLRDVAQNGQTDALPRIGMKPRRLKGLH 65
QY 56 AKIYAMHWATDSKLIYASASQDGKLIWDSYTTNKVHAIPLRSSWMTCAVAPSGNFVACG 115
Db 66 AKIYAMHWSTDRRLVYASASQDGKLIWDAYTTRKTHAIPLRSSWMTCAVAPSGNFVACG 125
QY 116 GLDMCSITNLSREGNVKVSRELTAHTGYLSCRFLLDNNITVSSGDTTCALMDIETGQ 175
Db 126 GLDNICSIYNSREGPTRVARELSGHSYLSGCRFINDRRIITSSGDMTCMLDIESGS 185
QY 176 QKTVEFGHTGDCMSLAVSP-DFNLIFSGACDASAKLMDVREGTCRQFTGHESDINAICF 234
Db 186 KVFTEFADHFGDVMSISINPTNNTFVSGACDAFAKIMDIRIGKSVQTFAGHESDINAICF 245
QY 235 FPNGEAICGSDDASCRLFDLRADQELICFSHESIICGITSVAFSLGRLPAGYDDFNCA 294
Db 246 FPDGNAFGTSDDTTCRLFDIRADRLSLNTYQSDQILCGITISVGFVSGRLPAGYDDFNCA 305
QY 295 NWDSMKSERVGLSGHNDNRVSCLGVTADGMAVATGSDSFLKIWN 339
Db 306 KWDVYLRGDKVGLSGHENRVSCLGVSNDGISLCTGSDSLKIVW 350

RESULT 9

Q9W3J1 PRELIMINARY; PRT; 358 AA.

AC Q9W3J1; 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CG10763 PROTEIN.
GN CG10763.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahler C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003443; AAF46336.1; -
 DR HSSP: P04901; 1TBG.
 DR FlyBase: FBgn0030011; CG10763.
 DR InterPro: IPR001632; -
 DR InterPro: IPR001680; -
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00319; GPROTEINB.
 DR PRINTS: PR00320; GPROTEINBPT.
 DR PROSITE: PS00678; WD_REPEATS; 3.
 DR SMART: SM00320; WD40; 1.
 DR Repeat: WD repeat.
 KW SEQUENCE 358 AA; 39354 MW; E9C6DEF91C503231 CRC64;

Query Match 53.5%; Score 967.5; DB 5; Length 358;
 Best Local Similarity 50.0%; Pred. No. 2.5e-82;
 Matches 170; Conservative 78; Mismatches 89; Indels 3; Gaps 2;

QY 3 EMEQLRQAEQLKKQIADARACADVTTLAEVSGLEVGRVQMRTRTLRGHLAKIYAMH 62
 Db 18 KMASLVREAENLKTLEERQKLVNDVLSNIAERLEQIAYVNIKPRKVLKGHQAQVLCCTD 77
 QY 63 WATDSKLLVSASQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNMCS 122
 Db 78 WSPDKRHITSSQDGRLLIWDFTTNKEHAVTMTPTWIMACAYAPSGNFVACGGLDNKVT 137
 QY 123 IYNLKSREGNVKVSRELTAHTGYLSCRFLLD-DNNIVTSSGDTTCALMDIETGQKTVFV 181
 Db 138 VYPTSDDEMAAKKRTVGTHTSYMSCCIYPSNDQILTGSGDSTCALMDVESGQLQSFH 197
 QY 182 GHTGDCMSLAVSPD-FNLFTSGACDASAKLMDVREGTCRQFTGTGHESDINALICFPNGE 239
 Db 198 GHSGDVMAIDLAPNETGNTFVSGSCDRMAFIWDRSGHVQSFEGHQSDVNSVKFHPCCD 257
 QY 240 AICTGSDSDASCRFLDLRADQELICFHSHEITIGTISVAFSLGRLIFAGYDDFNCNVWDS 299
 Db 258 AATGSDSDSCRLYDMKADREAVAFKESIIFGVNSVDFSVSGRLIFAGYNDYTVNLMDT 317
 QY 300 MKSERVGLISGHDNRVSLGVTADGMAVATGSDSFLKIW 339
 Db 318 LKSERVCLLYGHENKVCVQVSPDGTALSTGSDWTIRVW 357

RESULT 10
 Q9H9U9 PRELIMINARY; PRT; 395 AA.
 ID Q9H9U9
 AC Q9H9U9;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT 5L.
 GN GNBS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
 RT "Cloning and characterization of human G-protein beta 5L subunit.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF300650; AAC18444.1; -
 SQ SEQUENCE 395 AA; 43566 MW; E001B07FCFA587AD CRC64;

Query Match 52.5%; Score 949.5; DB 4; Length 395;
 Best Local Similarity 52.2%; Pred. No. 1.4e-80;
 Matches 178; Conservative 56; Mismatches 102; Indels 5; Gaps 3;

QY 4 MEQLRQAEQLKKQIADARACADVTTLAEVSGLEVGRVQMRTRTLRGHLAKIYAMH 63
 Db 54 LASLSEAESESLKGLIEERAKLHDELHOVAERVEALGQFVMTKTRTLKGHNKVLCDW 113
 QY 64 ATDSKLLVSASQDGLIWDSTYTNKVAIPLRSSWMTCAVAPSGNFVACGGLDNMCS 123
 Db 114 CKDKRRIVSSQDGRVIVWDSFTTNKEHAVTMTPTWIMACAYAPSGCAIACGGLDNKCSV 173
 QY 124 YNL--KSREGNVKVSRELTAHTGYLSCRFLLD-DNNIVTSSGDTTCALMDIETGQKTVF 180
 Db 174 YPLTFDKNENMAKKKSVAMHTNYLSACSFNTSDMQLTASGDCALMDVESGQLQSF 233
 QY 181 VGHTGD--CMSLAVSPDENLFTSGACDASAKLMDVREGTCRQFTGTGHESDINALICFPNG 238
 Db 234 HGHGADVLCLDAPSETGNTFVSGGCDKAMWDMRSGQCVQAFETHESDINSVRYPSG 293
 QY 239 EAICTGSDSDASCRFLDLRADQELICFHSHEITIGTISVAFSLGRLIFAGYDDFNCNVWD 298
 Db 294 DAFASGSDATCRFLDLRADREVAIYSKESIIIFGASSVDFSLGRLIFAGYNDYTVNLWD 353
 QY 299 MKSERVGLISGHDNRVSLGVTADGMAVATGSDSFLKIW 339
 Db 354 VLKGSRSVILFGHENRVSTLRVSPDGTAFCSGSDWDTLRVW 394

RESULT 11
 Q9NFZ1 PRELIMINARY; PRT; 346 AA.
 ID Q9NFZ1
 AC Q9NFZ1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GUANINE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT.
 OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Calliphoridae; Calliphora.
 OX NCBI_TaxID=7373;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EYE;
 RA Schulz S., Huber A., Schwab K., Paulsen R.;
 RT "A novel Ggamma isolated from Drosophila constitutes a visual G
 protein gamma subunit of the fly compound eye.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ250442; CAB76452.1; -
 DR InterPro: IPR000364; -

Query Match	45.48;	Score 820.5;	DB 10;	Length 377;
Best Local Similarity	48.18;	Pred. No. 1.5e-68;		

[illegible]

Db 127 LDSVCSIFNLSPTRDGNLNVSRMLSGHKGYSSCOYVPGEDTHLITGSGDQTCVLMWI 186
QY 172 ETGQOKTVE-----VGHTGDCMSLAVS-PDFNLFISGACDASAKIMDVREGT-CROPTFG 224
Db 187 TTGLRTSVFGEFQSGHTADVLISISNGSKLFEVSGSCDATALMDTRVARSVRTPHG 246
QY 225 HESDINACEFEPNGEALICGSDASCRLFLRADQELICFS---HESIICGITSVAFLS 281
Db 247 HEGDVNSVKEFPDGNFEGTSGEDGTCTRLDIRTGHQLOVYNQOHQDNEMAHVTSIAFIS 306
QY 282 GRLLFAGYDDFNCNVWDSMKSERV-----GILSGHNDNRVSLGVTADGMAVATGWSDFLK 337
Db 307 GRLLIAGYTGDCVYWDTLAKVYVNLGSLQNSHGRITCLGMSADGSLCTGSMWDTNLK 366
QY 338 IW 339
Db 367 IW 368

RESULT 14
Q9VW29 PRELIMINARY; PRT; 346 AA.
AC Q9VW29; 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
GN G-BETA-76C OR G-BETA-76C OR CG8770.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Ephydroidea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Relneer K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003516; AAF49124.1; -.
DR HSSP: P04901; ITBG.
DR FLYBase; FBgn0004623; G-beta-76C.
DR InterPro; IPR001632; -.
DR InterPro; IPR001680; -.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00319; GPROTEINB.
DR PRINTS; PR00320; GPROTEINBPT.
DR PROSITE; PS00678; WD_REPEATS; 1.
DR SMART; SM00320; WD40; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 346 AA; 38335 MW; E9B2D937EC3A707 CRC64;

Query Match 45.0%; Score 814; DB 5; Length 346;
Best Local Similarity 42.8%; Pred. No. 5.4e-68;
Matches 145; Conservative 81; Mismatches 111; Indels 2; Gaps 1;
QY 3 EMEQIRQEAQLKKQIADARKACADVTLAEVSGLEVGRVOMRTTRTLRGLAKIYAMH 62
Db 7 ETOKLYDEINGMIGKFKDDQKSKADCTLADKCGMDVYPKIRFSSKILKGINKVSVH 66
QY 63 WATDSKLVSASQDGLIWDSTTTNKVHAIPLRSSWMTCAVAPSGNFVACGLDNMCS 122
Db 67 FAGDSRHCVTSGSLDGKLIIMWTANKVQIIPLSAWMTVAVSPSGNFVACGMNQCT 126
QY 123 IYNLKSRE--GNVKSRELSAHTGYLSCREFLDNNIVTSSGDTTCALMDIETGQOKTVE 180
Db 127 VYDVNNRDASGVAKMKVLEMGEGFLSSCRFLDDGHLITSGDMKICHWLEKGVKTMDF 186
QY 181 VGHTGDCMSLAVSPDFNLFISGACDASAKIMDVREGTCTROTFTGHESDINACEFPNGEA 240
Db 187 NGHACDIAGLSLSPDKTYITGSVDTAKLMDVREGHKQMFEGHMDVSSVCYHPSPFG 246
QY 241 ICTGSDDASCRLFLRADQELICFSHESIICGITSVAFLSGLRLLFAGYDDFNCNVWDSM 300
Db 247 FASCSEDATARNYDLRADQIQAGYEPQKNTGFTSCALSTSGRYLMCGGIEGNVHSDTM 306
QY 301 KSERVGLSGHNDNRVSLGVTADGMAVATGWSDFLKIW 339
Db 307 KORHTGTLSGHENRITCISLCPNGMCLASTSMDQVRLW 345

RESULT 15
Q9FV61 PRELIMINARY; PRT; 377 AA.
AC Q9FV61; 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
GN HETEROTRIMERIC GTP-BINDING PROTEIN SUBUNIT BETA 1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SAMSUN; TISSUE=HAIRY ROOT;
RX MEDLINE=21002315; PubMed=11126570;
RA Ando S., Takumi S., Ueda Y., Ueda T., Mori N., Nakamura C.,
RT "Nicotiana tabacum cDNAs encoding alpha and beta subunits of a
RT heterotrimeric GTP-binding protein isolated from hairy root tissues."
RL Genes Genet. Syst. 75:211-221(2000).
DR EMBL: AF249743; AAG12330.1; -.
SQ SEQUENCE 377 AA; 40914 MW; 7052089F40A1707E CRC64;

Query Match 44.7%; Score 809; DB 10; Length 377;
Best Local Similarity 45.1%; Pred. No. 1.8e-67;
Matches 161; Conservative 72; Mismatches 98; Indels 26; Gaps 9;

```

0Y      4 MEOLROAEQOLKQIADARKACADVTTLAEIVSGLEV--GRVQMRTRFRLRGLAKIYAM 61
      :  ||:  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |  :  |
Db      17 VNDIREKLKQKRLQLDD-----TDSGYARSQCKTPVTFGPPTDLVCCRILOGHTGKVI 71
0Y      62 HMATDSKLLVASASODGKLIWMSYTTNKVHAIFPLRSSWVMTCAYAPSGNEVACGGIDNMC 121
      |  :  :  |||||:|:|:|  :  |  |  |  |  :  :  |||||:|:|  |||||:|
Db      72 DWTPEKNRIVASASODGRLIWMNALTSQKTHAIKLPICAWMTCAFSPSGQSVACGGLD 176
0Y      122 SIYNLKS---REGNVKYSRELSAHTGYLSCCRFL--DDNNIVTSSGDTTCALMDIETGOO 191
      ||:|  |  :  :  |  ||  |  |  |  |  |  |  :  :  :  :  |||||  |  ||  |  |
Db      132 SIFNLNSPIDKGDHNPVSRMLSGHKGYVSSCOYVPEDEDTLITSSGDTQCVLMDITTTGLR 229
0Y      177 KTFV-----VGHGDCMSLAV-SPDFNLFISGACDASAKLMDVREGT-CROTFTGHESDI 251
      :  :  :  |  ||  |  :  :  |  :  :  |  :  :  |  :  |  |  |  :  :  |  |  :
Db      192 TSVEGGEFQSGHTADVQSVSISSNPRLFVSGSCDTTACIMDTRVASAQRTEFYGHEDV 286
0Y      230 NAICEFPNGEALICTGSDDASCRLFDLRADOELICFSH---ESIICGITSVAFSLSGRLLE 311
      |  :  |  |  :  |  ||||  :  |||||:|  :  |  :  :  :  :  :  :  :  :  :  :  :
Db      252 NTVAFSPDGNRFGTGSEDEGTCLRLFDIRTHGLOLVYQPHGOGDIPHTVSMAFSISGRLEF 339
0Y      287 AGYDDENCNVWDSMKSERV---GILSGHDNRVSCLGVTADGMAVATGWSDFLKI 368
      |  :  :  |  ||:  :  :  |  :  :  |  :  |  :  |||  :  |  :  ||||  :  |||
Db      312 VGYNSGDCYVMDTLAKAVVNLGCVQNSHEGRISCLGLSADGSALCTGSMWDTNDKIM 368

```

Search completed: September 28, 2001, 10:34:07
Job time: 282 sec